		75 Seconds) updates/sec	
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	using sw model	October 14, 2005, 15:51:19; Search time 38.4375 Seconds (without alignments) 50.310 Million cell updates/sec	-10
Copyright (OM protein - protein search, using sw model	October 14, 2	US-10-614-959-10
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BLOSUM62 Gapop 10.0 , Gapext 0.5 29 1 TYAMH 5 Scoring table: Title: Perfect sc Sequence:

Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:* A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Query Result

Description	Aav79068 Anti-fact		~	Aag65570 Amino aci		9 HCV E1	7 Protein		Adn27332 Bacterial	Aag72483 Human OR-					ABD			Pepti	Aam33985 Peptide #	_	Human	Нишал	Human		Human	
ΩI	AAY79068	AAB14789	AAB14784	AAG65570	ABG76537	ABG76559	ABU24807	ABO77482	ADN27332	AAG72483	AAG71475	ADR10293	AAY50844	AAY50835	AAB14781	AAB14782	AAM82576	ABB40299	AAM33985	AAM73798	AAM61093	ABG55546	ABG43685	AAU18208	ABG92629	
8	Э	m	m	4	ß	S	9	7	æ	4	4	80	m	m	ო	m	4	4	4	4	4	4	2	4	2	
Match Length DB	S	7	12	120	121	128	206	258	278	307	321	531	069	9	703	703	46	67	67	67	67	67	67	79	79	
Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	
Score	53	29	29	29	53	53		53		59	53	29	53	29	29	29	56	56	26	56	26	26	56	26	26	
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Adc25346 Human ext Abg68752 Cytochrom Abg68756 Cytochrom Ade08218 Novel pro Ade08218 Novel pro Adb91152 Herbicida Adb91152 Herbicida Adb91152 Human pro Abb4642 Human pro Abb46910 Lieteria Abb49910 Lieteria Abb49910 Lieteria Abb49910 Lieteria Abb49910 Lieteria Abb49910 Lieteria Adg66693 Bangle ch Abb49910 Lieteria Adg68693 Bangle ch Abg91621 C glutami Abg91621 Ribbiell Adf68001 Bacterial Ado47342 Rabbit cy Ade57186 Human Cyt Ade57186 Human Pro Ade57186 Human Pro Ade57186 Human Pro	
ADC25346 ABG68752 ABP01422 ABC8756 ADE08218 ADE08219 ADB1152 ADA55412 ADA55412 ABH40910 ABH40910 ABH40910 ABH40910 ABH40910 ABH40910 ABH409103 AAC30014 ABC6102 ADC6102 ADC6102	
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
24444444444444444444444444444444444444	

ALIGNMENTS

Anti-factor IX/IXa antibody H chain V domain CDR1 amino acid sequence. AAY79068 standard; peptide; 5 AA. (first entry) 12-JUN-2000 AAY79068; RESULT 1 AAY79068 ID AAY7

Complementarity determining region 1; CDR1; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999;

28-AUG-1998; 98US-0098233P. 03-MAR-1999; 99US-0122767P.

(GETH) GENENTECH INC

Kirchhofer D; Hass PE, Judice JK, Devaux B, Eaton DL, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the heavy chain variable domain of a human anti-factor IX/Ixa Gla domain antibody. Pactor IXA/Ixa da vitamin K dependent plasma serine procease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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3 TYAMH

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Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum pH of about 8.5. The glutaminases catalyse the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodsruffs such as soy sauce and miso. Sequences AABA1787-1814789 represent fragments of Aspergillus oryzae KBN616 glutaminase which were used as the basis for the design of degenerate PCR primers AAA72206, AAA72207 and AAA72209. These primers were used in the isolation of genomic DNA encoding Aspergillus oryzae
                                                                                                                                                                                                                                                                 ö
           the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infartronhosis, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
platelets. Compositions comprising the antibodies are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glutaminase, Aspergillus oryzae KBN616; glutamic acid synthesis;
fermentation, foodstuff production, miso, soy sauce, peptide fragment;
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.
                                                                                                                                                                                                                            ; Score 29; DB 3; Length 5;
; Pred. No. 1.8e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 25; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14789 standard; peptide; 7 AA.
                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-00347127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-477931/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus oryzae.
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KBN616 (AAA72204)
                                                                                                                                                                                                                                                                                                       1 TYAMH 5
                                                                                                                                                                                                                                                                                                                                        TYAMH 5
                                                                                                                                                                                              Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB14789;
                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                AAB14789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                          SEQ ID NO:6.
                                                                                                                                         Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
fermentation; foodstuff production; miso; soy sauce;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 29; DB 3; Length 12; 100.0%; Pred. No. 6.5; ive 0; Mismatches 0; Indels
                                                                                                               Aspergillus oryzae KBN616 glutaminase peptide fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene library; immunoglobulin; antibody library; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of protein seq Id No. 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG65570 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 9; 27pp; Japanese.
                        AAB14784 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                           98JP-00347127.
                                                                                                                                                                                                                                                                                            98JP-00347127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                   06-DEC-2000 (first entry)
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5; Conservative
                                                                                                                                                                          V8 protease digestion.
                                                                                                                                                                                                                                                                                                                                                                      (ICHI-) ICHIBIKI KK.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-477931/42
                                                                                                                                                                                                       Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TYAMH 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 AA;
                                                                                                                                                                                                                                    JP2000166547-A.
                                                                                                                                                                                                                                                                                                                           07-DEC-1998;
                                                                                                                                                                                                                                                                                               07-DEC-1998;
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Best Local S:
Matches 5,
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                                                      AAB14784;
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RESULT 3
               AAB14784
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Gaps

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100.0%; Score 29; DB 3; Length 7; 100.0%; Pred. No. 1.8e+06; cive 0; Mismatches 0; Indels

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Query Match Best Local Similarity Matches 5; Conserv

Sequence 7 AA;

Gaps

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Homo sapiens

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The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) B1 antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from a combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV B1 or B2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABC76513-ABG76568 represent human monoclonal antibodies against HCV B1 antigen
comprising a human monoclonal antibody against hepatitis C virus or E2 antigen, useful for treating or preventing HCV infection.
                                                                                                 The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) B1 antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV B1 or E2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABG75513-ABG75568 represent human monoclonal antibodies against HCV E1 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, HCV; hepatitis C virus, El antigen, monoclonal antibody, vaccine, hepatotropic, Fab, hypervariable region, E2 antigen, antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) \rm El or \rm E2 antigen, useful for treating or preventing HCV infection.
                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 29; DB 5; Length 121; 100.0%; Pred. No. 73; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV El antigen monoclonal antibody #47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 52-53; 64pp; English.
                                                            Disclosure; Page 36; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG76559 standard; protein; 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JAN-2001; 2001US-0260889P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drakenberg K, Persson MAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
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  Vaccine con (HCV) El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; HCV; hepatitis C virus; El antigen; monoclonal antibody; vaccine; hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
                                                                                                                                                                                                                                                                                                                                                              Producing gene libraries and antibody libraries, involves selecting a
light chain that binds to a heavy chain product to produce a functional
formation, and producing a gene library of the light chain variable
                                                                                                                                                                                                                                               Takahashi M;
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                                                                                                                                                                                                                                           Shinohara M,
                                                                                                                                                                                                                                           Iba Y, Morino K,
                                                                                                                                                                                               (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV El antigen monoclonal antibody #25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examples; p 171; 181pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KARO-) KAROLINSKA INNOVATIONS
                                                                                                            22-FEB-2001; 2001WO-JP001298
                                                                                                                                                        22-FEB-2000; 2000JP-00050543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Persson MAA;
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                                                                                                                                                                                                                                        Akahori Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                          Shiraki K;
                                                                                                                                                                                                                                                                                                     WPI; 2001-565420/63
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH47734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 120 AA;
                            WO200162907-A1
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                                                                                                                                                                                                                                        Kurosawa Y,
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                                                                     30-AUG-2001
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                                                                                                                                                                                                                                                              Okuno Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                 regions.
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a pronoter operably linked to the nucleic acid
cenceding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
cantisense nucleic acid; (4) an antibody capable of specifically binding
cantisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contiferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
cc proliferation, or that inhibite cellular proliferation of the gene product or that has an activity against a biological pathway
cc required for proliferation-required gene or its gene product lies
cc pathway in which he test compound that inhibits proliferation of an
compound's activity; (11) a culture comprising strains in which the gene
cc product is overexpressed or underexpressed; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
cc product is overexpressed or underexpressed; (12) determining the extent
cc owhich each of the strains is present in a culture or collection of
ct to which each of the strains is present in a culture or collection of
ct proliferation of an organism. The antisense nucleic acids required
cf for cellular proliferation to isolate candidate molecules for rational
cf for cellular proliferation for for screening homologous nucleic acids
crips are acids
crips and discovery programs, or for screening homologous nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                   Gaps
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen KL,
Forsyth RA,
                   IndelB
                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #10334.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 52731; 1766pp; English.
                   Mismatches
  Pred. No.
                                                                                                                                                                                                       ABU24807 standard; protein; 206 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362851.
06-WAR-2002; 2002US-0362699P.
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                       (first entry)
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                       5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-029926/02
Best Local Similarity
Matches 5, Conserv
                                                                                                   32 TYAMH 36
                                                           1 TYAMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-029926
N-PSDB; ACA28677
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                                                                                                                                                                                                                                                                                       19-JUN-2003
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                                                                                                                                                                                                                                               ABU24807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang Wall
                                                                                                                                                              RESULT 7
                                                                                                                                                                                   ABU24807
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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and polymucleotides encoding them. The sequences are useful in diagnosis and polymucleotides encoding them. The sequences are useful in diagnosis and prophylaxis and treatment of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a compound, such as a polymeptide, or fetctive antibacterial targets, as targets for antibacterial durgs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed production of production 
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required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment o pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                     100.0%; Score 29; DB 6; Length 206; 100.0%; Pred. No. 1.3e+02; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 26228; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polypeptide #9657,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO77482 standard; protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0074788P.
98US-0094190P.
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                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-615309/58
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      30 TYAMH 34
                                                                                                                                                                                                                                                                                                                                                     1 TYAMH 5
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                                                                                                                                                                                            Sequence 206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 258
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us-10-614-959-10.rag

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Gaps ö

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to prowide for expression of a polymuclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant that may no method of producing a plant with the recombinant DNA construct and growing the transforming a plant with the polymiclectide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of homologous recombination, modification of carbohydrate, nitrogen or content, improved yield by modification of photosynthesis or by phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production or improved galactomannan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; berbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
Query Match
100.0%; Score 29; DB 7; Length 258; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 9985; 122pp; English.
                                                                                                                                                                                                                                ADN27332 standard; protein; 278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hinkle GJ, Slater SC,
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                                                                                                                                                                                                                                                                                                                                                             Bacterial polypeptide #9985
                                                                                                                                                                                                                                                                                                                 02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-061375/06
                                                                                                                          201 TYAMH 205
                                                                                  1 TYAMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAOY/)
                                                                                                                                                                                                        RESULT 9
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The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR) like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation. The polymucleotides can be used in screening for olfactory agonists and artagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                           ö
production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, olfactory receptor; OR; primary scent determination;
secondary scent determination; polypeptide library; odour receptor;
scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
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                                                                                                                                     Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
                                                                                                                                                                       0; Indela
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                                                                                                                               Query Match
100.0%; Score 29; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 1455-1456; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                        AAG72483 standard; protein; 307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-290713/30
                                                                                                                                                                                                                                             220 TYAMH 224
                                                                                                                                                                                                        1 TYAMH S
                                                                                          Sequence 278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                               AAG72483;
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Matches
                                                                                                                                                                                                                                                                                                     RESULT 10
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DB 4; Length 307;

100.0%; Score 29;

Sequence 307 AA;

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New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                          human; oligo-capping method; diagnostic marker; gene therapy; ostcoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emontjonal reaction; fear response; panic; ostcopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                             Human protein useful for treating neurological disease Seq 3799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 3799; 2686pp; English.
                                                                                                                                                                                                                                                                                                                                                  (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                .2-FEB-2004; 2004EP-00003145.
                                                                                                                                                                                                                                                                                                          14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
                                       04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-583265/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADR08337
                                                                                                                                                                   tranquiliser.
                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                         EP1447413-A2
                                                                                                                                                                                                                                                      18-AUG-2004.
              ADR10293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining the determining differences in the olfactory faculties of different
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                                                    Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuchs T,
                                                                                                                                                                                                                            Human olfactory receptor polypeptide, SEQ ID NO: 1156.
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  Pred. No. 1.9e+02;
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                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 674-675; 1857pp; English.
                                                                                                                                             AAG71475 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
  100.08;
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bellenson J, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-290713/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIGI-) DIGISCENTS.
                                                                        154 TYAMH 158
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                                             1 TYAMH 5
                                                                                                                                                                                                                                                                                                                                            WO200127158-A2
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                        19-APR-2001
                                                                                                                                                                         AAG71475;
                                                                                                                   RESULT 11
                                                                                                                                AAG71475
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Otsuki

T, Isono Y, Sugiyama T, Irie R;

Nishikawa Nagai K,

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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to molecules and the encoded proteins thereof. Specifically, it refers to conda clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to antibodies, antisense molecules and siRNAs that can all be used to bind to antibodies are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating ostcoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, disease, parkinson's disease, dementia, short memory and various cancers, for treating emotional reaction, fear response and panic. Accordingly, they exhibit ostcopathic, neuroprotective, nootropic, antiparkinsonian, cycostatic and tranquiliser activities. This sequence is not given in the sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY50844 standard; protein; 690 AA.
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5; Conservative
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Best Local S
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ID AAY5
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Gaps

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ADR10293 standard; protein; 531 AA.

RESULT 12 ADR10293 ID ADR10

169 TYAMH 173

1 TYAMH 5

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Glutaminase; decomposition; glutamine; glutamic acid; ammonia; taste enhancer; seasoning; sauce; paste.
                                                                                                                                                                              Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
                                                                        1. .20
/label= signal_peptide
21. .690
                                                                   Location/Qualifiers
                         A. oryzae glutaminase protein #2.
                                                                                                                                          98JP-00258974.
98JP-00292443.
99JP-00089157.
                                                                                                                         99WO-JP002455
                                                                                                                                    98JP-00134080
            (first entry)
                                                                                                                                                                   (AJIN ) AJINOMOTO CO INC.
                                                      Aspergillus oryzae.
            24-FEB-2000
                                                                                                WO9960104-A1
                                                                                                                        12-MAY-1999;
                                                                                                                                           11-SEP-1998;
14-OCT-1998;
                                                                                                                                    15-MAY-1998;
                                                                                                            25-NOV-1999
                                                                                                                                                      30-MAR-1999;
                                                                        Peptide
                                                                                    Protein
```

Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes. WPI; 2000-053292/04. N-PSDB; AAZ43684.

Example 3; Page 52-55; 74pp; Japanese.

This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutaminase and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and partes as well as other seasoning materials. The gene thus obtained DNA fragments from genome and collation providing the gene-containing novel strain of an subsequently modified glutaminase-producing breed. The nidulans, and subsequently modified glutaminase-producing breed. The secreting ability. This sequence represents the A. oryzae and encerting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention

Sequence 690 AA;

Gaps ö 100.0%; Score 29; DB 3; Length 690; 100.0%; Pred. No. 4.5e+02; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 5; Conservative

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AAY50835 standard; protein; 690 AA

RESULT 14

AAY50835;

24-FEB-2000 (first entry) AAY50835 ID AAY5 XX AC AAY5 XX DT 24-F XX DE A. c

A. oryzae glutaminase protein #1

Glutaminase; decomposition; glutamine; glutamic acid; ammonia; taste enhancer; seasoning; sauce; paste.

Aspergillus oryzae.

1. .20 /label= signal_peptide 21. .690 Location/Qualifiers Pept 1de

WO9960104-A1 Protein

12-MAY-1999;

99WO-JP002455

98JP-00134080. 98JP-00258974. 98JP-00292443. 99JP-00089157. 15-MAY-1998; 11-SEP-1998; 14-OCT-1998; 30-MAR-1999;

(AJIN) AJINOMOTO CO INC.

Kitamoto K; Koibuchi K, Nagasaki H, Yuasa A, Kataoka J,

WPI; 2000-053292/04. N-PSDB; AAZ43677.

Aspergillus oryzae-originated glutaminase and partial amino-acid sequences for enhancing taste particularly in glutamic acid-converting food processing to make e.g. seasoning sauces and pastes.

Claim la; Page 41-44; 74pp; Japanese.

This invention describes a novel glutaminase enzyme isolated from Aspergillus oryzae which catalyses the decomposition of glutamine to glutamic acid and ammonia. The purified glutaminese and determined partial amino-acid sequence can be used for enhancing taste particularly in glutamic acid-converting food processing to give e.g. seasoning sauces and pastes as well as other seasoning materials. The gene thus obtained can be applied as probe for hybridization providing the gene-containing DNA fragments from genome and cDNA libraries of A. oryzae and A. nidulans, and subsequently modified glutaminase-producing breed. The novel strain of A. oryzae is a highly active because of its somatic secreting ability. This sequence represents the A. oryzae glutaminase enzyme described in the method of the invention

Sequence 690 AA;

Gapa ö Ouery Match
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels

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1 TYAMH 5

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423 TYAMH 427

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AAB14781 standard; protein; 703 AA.

06-DEC-2000 (first entry)

AAB14781;

Aspergillus oryzae KBN616 glutaminase.

Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis; fermentation; foodstuff production; miso; soy sauce.

Aspergillus oryzae

```
This sequence represents a novel glutaminase from Aspergillus oryzae KBN616. The invention relates to two novel glutaminases (AAB14781, AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which have molecular weights of approximately 73 kD (as determined by gel filtration). The enzymes have an optimum temperature of approximately 50 degrees Celsius, and an optimum ph of about 8.5. The glutaminases catalyse the conversion of L-glutamine to L-glutamic acid, and may be used in the production of fermented foodstuffs such as soy
            Location/Qualifiers
34. .703
/note= "Mature glutaminase; specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

100.0%; Score 29; DB 3; Length 703;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            A new glutaminase and its preparation.
                                                                                                                                                                                                                                                                                                                           Claim 2; Page 15-17; 27pp; Japanese.
                                                                                                                                       98JP-00347127.
                                                                                                                                                                    98JP-00347127.
                                                                                                                                                                                                  (AICH-) AICHIBIKI KK.
                                                                                                                                                                                                                                             WPI; 2000-477931/42.
N-PSDB; AAA72204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 703 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sauce and miso
                                                                            JP2000166547-A.
                                                                                                                                       07-DEC-1998;
                                                                                                                                                                    07-DEC-1998;
                                                                                                          20-JUN-2000
                Key
Protein
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Gaps

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Search completed: October 14, 2005, 16:12:37 Job time : 42.4375 secs

||||| 436 TYAMH 440 1 TYAMH 5

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October 14, 2005, 16:00:04; Search time 9.84375 Seconds (without alignments) 37.917 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
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US-10-614-959-10 29 1 TYAMH 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Query				
No.	Score	Match	Match Length	BB	ΔI	Description
7	59	100.0	ß	4	US-09-383-667-10	Sequence 10, Appl
~	53	100.0	118	4	US-09-232-290-45	45
e	59	100.0	258	4	US-09-252-991A-26228	2622
4	53	100.0	069	4	US-10-262-083-2	
Ŋ	53	100.0	069	4	US-10-262-083-18	1 8
9	56	89.7	108	4	US-09-270-767-35497	354
7	56	89.7	108	4	-60	5071
ω	56	89.7	454	4	-60-	1028
0	56	89.7	455	4	-60-	8288
21	56	89.7	502	4	-60	Sequence 5992, Ap
11	56	89.7	507	4	-60	7091
12	56	89.7	544	4	-60	699, A
	56	89.7	544	4.	27	270.
14	22	86.2	S	-		21.
15	52	86.2	S	٣	US-08-918-148-26	26.
16	52	86.2	S	4	US-09-383-667-21	21.
17	25	86.2	S	4	US-09-138-091A-26	26.
18	25	86.2	2	4	US-09-424-840B-34	'n
19	22	86.2	S	4	US-09-424-840B-91	91,
20	22	86.2	S	4	US-09-830-748B-10	10,
21	52	86.2	38	-	US-07-977-630-67	ø
22	25	86.2	28	4	US-09-270-767-38850	3885
23	52	φ	58	4	US-09-270-767-54067	Sequence 54067, A
24	22	9	98	ч	US-08-211-202-118	
25	22	86.2	114	4	US-09-726-219A-222	222
	52	ø	116	٦	US-08-211-202-141	141
27	22	86.2	117	ო	US-08-545-809A-91	91

Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 145, Appl Sequence 14399, A Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 12, Appl Sequence 13, Appl
US-09-025-769B-24 US-09-490-070A-24 US-09-490-133-24 US-09-490-133-24 US-08-545-809A-145 US-08-545-809A-145 US-08-248-796A-14399 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-561-521-13 US-08-759-804A-46 US-09-227-693-46 US-08-759-804A-11 PCT-US95-01219-12
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Sequence 45, Application US/0923290A

Sequence 45, Application US/0923290A

Sequence 45, Application US/0923290A

Sequence 45, Application

General No. 6815540

APPLICANT: PLUCKTHUN, ANDREAS

APPLICANT: NIEBA, LARS

APPLICANT: NIEBA, LARS

TITLE OF INVENTION: IMMUNGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH

FILLE REFERENCE: MORPHO/7

FILLE REFERENCE: MORPHO/7

CURRENT APPLICATION NUMBER: US/09/232,290A

CURRENT FILING DATE: 1999-01.15

EARLIER APPLICATION NUMBER: PCT/EP96/02230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gарв
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US-09-383-667-10

| US-09-383-667-10
| Sequence 10, Application US/09383667
| Patent No. 6624283
| GENERAL INFORMATION:
| APPLICANT: Adams, Camelia W. |
| APPLICANT: Adams, Camelia W. |
| APPLICANT: Baton, Dan L. |
| APPLICANT: Hass, Philip E. |
| APPLICANT: Mass, Philip E. |
| APPLICANT: Suggett, Shelley |
| TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies |
| TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies |
| TITLE OF ILLNG DATE: 1999-08-26 |
| CURRENT APPLICATION NUMBER: US/09/383,667 |
| CURRENT FILING DATE: 1998-08-26 |
| EARLIER FILING DATE: 1999-03-03 |
| SEALIER PELLING DATE: 1999-03-03 |
| SEALIER PILING DATE: 1999-03-03 |
| SEALIER PILING DATE: 1999-03-03 |
| SEALIER PILING DATE: 1999-03-03 |
| TYPE: PRT |
| ORGANISM: Homo mapiens |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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1 TYAMH 5
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RESULT 5

193-102-262-083-18

195-102-262-083-18

196-262-083-18

196-262-083-18

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196-262-083-18

196-262-083-18

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196-262-083-18

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196-262-083-18

196-262-10-0-PCT

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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERBNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Local Similarity 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            100.0%; Score 29; DB 4; Length 690; 100.0%; Pred. No. 1.1e+02; ative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VERSION 3.1
SEQ 100 2
LENGTH: 690
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18
                                                                                                                                                                                                                , ORGANISM: Aspergillus oryzae US-10-262-083-2
                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: YUASA, Ari
APPLICANT: YUASA, Ari
APPLICANT: KITAMOTO, Katsuhiko
APPLICANT: KITAMOTO, Katsuhiko
APPLICANT: KITAMOTO, Katsuhiko
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing I
FILE REFERENCE: 1994340S-822-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262,083
CURRENT FILING DATE: 2000-11-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-10-14
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100.0%; Score 29; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0: Indela
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Patent No. 6830905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228
                        EARLIER FILING DATE: 1996-05-23
                                                NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 118
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 TYAMH 205
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                                                                                                                                                                                                      ; ORGANISM: Murine US-09-232-290-45
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILLE OF INVENTION: DATE: 2000-04-05
FILLE REFERENCE: 2000-04-05
FILLE REPORT APPLICATION NUMBER: US 60/128,706
FRIOR APPLICATION NUMBER: US 60/128,706
FRIOR PRIOR DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR FILING SARA
FILENGTH: 455
FRIOR PROCESS B344
FRIO
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| Sequence 5992, Application US/09949016
| Patent No. 681239
| GENERAL INPORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| PRIOR APPLICATION NUMBER: 60/231,768 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: PSESEE FOR Windows Version 4.0 |
| SEQ ID NO 5992
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Sequence 7091, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 3.6e+02;
1; Mismatches 0;
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80.0%; Pred. No. 3.9e+02;
iive 1; Mismatches 0;
                                                                                                                                 US-09-543-681A-8288
; Sequence 8288, Application US/09543681A
; Patent No. 6605709
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80.0%;
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Best Local Similarity 80.0*
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Best Local Similarity 80.0
                  152 TYALH 156
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225 TYALH 229
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-949-016-5992
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Patent No. 6610836
GENERAL INVENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: 08/09/489,039A

CURRENT FILING DATE: 2000-01-27

CURRENT FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10284

LENGTH: 454
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US-09-270-767-50714
US-09-270-767-50714
Sequence 5.0714, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFURARE: PatentIn Ver. 2.0
SEQ ID NO 50714

LENGTH: 108
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Pred. No. 85;
1; Mismatches 0; Indels
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80.0%; Pred. No. 85;
live 1; Mismatches
                                                                                                                                                                                ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50714
                                                                                                                    ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35497
LENGTH: 108
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0°
Matches 4; Conservative
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64 TYALH 68
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64 TYALH 68
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US-09-489-039A-10284
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US-08-264-093-21
Sequence 21, Application US/08264093
Setent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Aldout & Maybee
STRRET: 2300 Richmond-Adelaide Centre
STRRET: 2300 Richmond Adelaide Centre
STRRET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                   Score 26; DB 4; Length 544;
Pred. No. 4.3e+02;
1; Mismatches 0; Indels
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MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC COmpatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCII Editor CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRILING DATE:
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/ASENT INDEMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELECHORE: (416) 362-0823
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270
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TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             89.7%;
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Best Local Similarity 80.0°
SOFTWARE: PERL Program SEQ ID NO 270
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
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Matches 4, Conserv
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US-08-918-148-26
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; Sequence 699, Application US/09976594
; Patent No. 6673549
; GENERAL INPORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEG ID NOS: 1143
; SOFTWARE: PERL PROGram
; SEQ ID NO 699
; LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
; NAWA, VITEL OF SET OF S
      IIILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 4e+02;
1; Mismatches 0; Indels
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CTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
US-09-976-594-699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.7%; Score 26; DB 4; I
80.0%; Pred. No. 4.3e+02;
tive 1; Mismatches 0
                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 7091
LENGTH: 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.7%;
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Best Local Similarity 80.۰
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Best Local Similarity
Matches 4; Conserv
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485 TYALH 489
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US-09-976-594-699
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Page 5
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Sequence 26, Application US/08918148A

Patent No. 6342220

GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: Garter, Paul J.
APPLICANT: Garter, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: 10979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 26
LENGTH: S
TYPE: PRT
OGGANISM: artificial
FEATURE:
NAME/KEY: 10D108cFv, 12B5scFv VH CDR1
COCATION: 1-5
COCHION: 1-5
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Search completed: October 14, 2005, 16:22:00 Job time : 10.8438 secs

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Query Match 86.2%; Score 25; DB 3; Length 5; Best Local Similarity 80.0%; Pred. No. 4.1e+05; Matches 4; Conservative 0; Mismatches 1; Indels

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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USOB_NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                             US-10-614-959-10
29
1 TYAMH 5
                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 64, Appl	91,	Sequence 12. Appl	25,		Sequence 47, Appl	311				Sequence 34, Appl
ΩΙ	US-10-989-462-64	US-10-468-543-91	US-11-003-819-12	US-10-466-242-25	US-10-989-462-7	US-10-466-242-47	US-10-425-115-311733	US-10-424-599-231272	US-10-425-115-211694	US-10-282-122A-52731	US-10-989-462-34
ВВ	18	15	20		18	16	16		16	15	18
% Query Match Length DB ID		11	119	121	123	128	137	151	158	206	257
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	29	29	29	29	29	29	29	29	29	29	29
Result No.	-	7	Э	4	co	9	7	80	9	10	11

Seguence 9985. Ap	Sequence 2,	18	~	18	35	Sequence 254	Seguence 186	Sequence 363	Sequence 217	2 Sequence 186	4 Seguence 1	Sequence 246	Sequence 4	Sequence 19087	Sequence 27191	Sequence 19274	Sequence	Sequence 24558	Seguence 193	Sequence 193,	Seguence 48571	3 Sequence 21419	Seguence 2683	3 Sequence 22765	14 Seguence 14364	3 Seguence	Sequence 2980, A	Sequence 2053,	Sequence 205	65 Sequence 45565,	e 42,	3768	5177
US-10-369-493-	US-10-262-083-2	US-10-262-083-	US-10-851-337-	US-10-851-337-1	US-10-468-543-3	US-10-425-115-	US-10-425-115-1	US-10-425-115-	US-10-424-599-	US-10-424-599-1	US-10-437-963-	US-10-425-115-2	US-09-864-761-4	US-10-424-599-	US-10-425-11	US-10-424-599-1	US-10-424-59	US-10-424-599-2	US-09-764-846-15	US-10-091-483-1	US-10-767-701	US-10-42	US-10-425-115-2	US-10-424-599-2	US-10-424-599-	US-10-767-701-	US-10-094-749-	US-09-88	US-10-293-418-205	US-10-282-122A-45	US-10-831-070-	-09-738-626-37	-09-738
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-10-989-462-64

Sequence 64, Application US/10989462

Publication No. US20050220795A1

GENERAL INFORMATION:
APPLICANT: Wittrup, K. Dane
APPLICANT: Wittrup, K. Dane
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFRENCE: 01997-329001
CURRENT APPLICATION NUMBER: US 40/509,462
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR PILING DATE: 2004-04-19
SOFTWARE: FRANCEOF OF WINDOWS VERSION 4.0
SEQ ID NOS: 319
SOFTWARE: FRANCEOF OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indele
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100.0%; Score 29; DB 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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; Sequence 25, Application US/10466242;
; Publication No. US20040208887A1
; GENERAL INFORMATION:
    APPLICANT: Drakenberg, Katarina
    APPLICANT: Drakenberg, Katarina
; APPLICANT: Drakenberg, Katarina
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
    TILE REFERENCE: 0380-02480500;
    CURRENT APPLICATION NOWBER: US/10/466,242
    CURRENT FILING DATE: 2004-01-16
    PRIOR APPLICATION NOWBER: PT/SE02/00044
    PRIOR PLING DATE: 2002-01-14
    NUMBER OF SEQ ID NOS: 56
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 25
    LENGTH: 121
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100.0%; Score 29; DB 18; Length 123;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 29; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels (
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1Sequence 7, Application US/10989462

1 Sequence 7. Application US/10989462

2 Bedication No. US20050220795A1

3 GENBEAL INFORMATION:

4 APPLICANT: Wittrup, K. Dane

5 APPLICANT: Wittrup, XR Andy

1 TITLE OF INVENTION: THEREOF

7 ITLE OF INVENTION INVERSE: 20 60/550,114

7 PRIOR FILING DATE: 2003-11-14

7 PRIOR FILING DATE: 2003-11-14

7 PRIOR FILING DATE: 2004-04-19

8 NUMBER OF SEQ ID NOS: 319

8 SOFTWARE: FASESEQ for Windows Version 4.0

8 SEQ ID NO 7

8 LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS-10-466-242-47

Sequence 47, Application US/10466242

Publication No. US2004020887A1

PENERAL INFORMATION:

APPLICANT: Drakenberg, Katarina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 TYAMH 35
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                                                                                               Sequence 91, Application US/10468543

Fublication No. US20040091938A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Irimura, Tatsuro
APPLICANT: Yim, Mijung
APPLICANT: Ono, Takashi
APPLICANT: Ono, Takashi
CURRENT PILING DATE: 2001-08-20
CURRENT APPLICATION NUMBER: US/10/468,543
CURRENT FILING DATE: 2001-04-221
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LUNGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/11003819

Sequence 12, Application No. US2005015833A1

Sequence 12, Application No. US2005015833A1

GENERAL INFORMATION:

APPLICANT: Evans, Elizabeth E.

APPLICANT: Sahasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

APPLICANT: Salasrabudhe, Deepak M.

TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens

TITLE OF INVENTION: Methods of Killing Tumor Cells

TITLE OF INVENTION: WIMBER: US/11/003,819

CURRENT APPLICATION NUMBER: US 60/256,572

PRIOR FILING DATE: 2003-12-04

PRIOR FILING DATE: 2003-12-23

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn version 3.3

SEQ ID NO 12

LENGTH: 119

TAVER: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 71;
vative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 29; DB 15; Length 11; Best Local Similarity 100.0%; Pred. No. 7.2; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5, Conservative
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COCANISM: Homo sapiens
US-11-003-819-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 TYAMH 35
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US-10-466-242-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Gaps

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Gaps

8

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 211694
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 29; DB 15; Length 151; 100.0%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 29; DB 16; Length 158; 100.0%; Pred. No. 94;
                                                                                                                                                   TYPE: PRT
ORCANISM: Glycine max
FEATURE:
NAMBYKEY: unsure
LOCATION: (1)...(151)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT3847_50860C.1.pep
US-10-424-599-231272
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US-10-425-115-211694
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NAME/KEX: unsure
(1)..(158)
OTHER INFORMATION: unsure at all xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Sequence 52731, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Chery1
APPLICANT: Malone, Chery1
APPLICANT: Applicant: Ohlsen, Kari
APPLICANT: Cyakind, Judith
APPLICANT: Applicant: Jakind, Judith
APPLICANT: Mall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 211694, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                  CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 231272 LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Zea mays
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US-10-425-115-311733
US-10-425-115-311733
Sequence 311731, Application US/10425115
Sequence 311731, Application No. US20040214272A1
SENERAL INFORMATION:
APPLICANT: Expension Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO: 31733
LENGISH: 137
LENGISH: 137
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Covalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
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APPLICANT: Persson, Mats
TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
FITLE OF INVENTION: Materials and methods for treatment of hepatitis C
FILE REPERSIVE: 0180-P01243800
CURRENT PILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: DCT/SE02/00044
PRIOR RILING DATE: 2002-01-14
PRIOR FILING DATE: 2002-01-17
FILING DATE: PRI NOS: 56
SOFTWARE: PATENTIN VERSION 3.1
FIRING NO 47
FIRIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 29; DB 16; Length 137; Best Local Similarity 100.0%; Pred. No. 82; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(128)
; OTHER INFORMATION: Clone 2b:5 VH
US-10-466-242-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 TYAMH 36
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16 TYAMH 20
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034
FULE REPERENCE: ELITAA.034
FULE REPERENCE: ELITAA.034
PRIOR APPLICATION NUMBER: 05/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,579
PRIOR APPLICATION NUMBER: 60/25,655
PRIOR APPLICATION NUMBER: 60/25,636
PRIOR PPLING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
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Sequence 3.4. Application No. US20050220795A1

GENERAL INFORMATION:
APPLICANT: Wittury, K. Dane
APPLICANT: Yeung, Yik Andy
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT APPLICATION NUMBER: US/10/989,462
CURRENT APPLICATION NUMBER: US 60/520,114
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2004-04-19
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PRESERE 2004-04-19
SEQ ID NO 34
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29; DB 18;
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Clostridium botulinum US-10-282-122A-52731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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US-10-262-083-2
Sequence 2, Application US/10262083
Sequence 2, Application US/10262083
Fublication No. US20030170670A1
GENERAL INFORMATION:
APPLICANT: KOISMATION:
APPLICANT: WORSA, Ari
APPLICANT: KATAOKA, Jiro
APPLICANT: WORSAN: US/10/262,083
CURRENT APPLICATION NUMBER: US/10/262,083
CURRENT FILING DATE: 2000-11-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1999-03-10
PRIOR PLILING DATE: 1999-03-10
PRIOR FILING DATE: 1999-03-10
PRIOR PLING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                                         US-10-369-493-9985

j Sequence 9985, Application US/10369493

j Publication No. US20030233675A1

j APPLICANT: Gao, Yongwei

j APPLICANT: Slater, Steven C.

j APPLICANT: Gladman, Barry S.

j APPLICANT: Chen, Xianteng

j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

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; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-9985
           Mismatches
           ö
           5, Conservative
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31 TYAMH 35
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                Matches
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us-10-614-959-10.rapb

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1998-10-14
PRIOR PILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 14, 2005, 17:00:41 Job time : 36.5469 secs
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; ORGANISM: Aspergillus oryzae
US-10-851-337-2
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Sequence 18, Application US/10262083

Sequence 18, Application US/10262083

Sequence 18, Application No. US20030170670A1

GENERAL INFORMATION:

APPLICANT: WIGAGAKI, Hiroaki

FRICK REEKENCE: 19943049-62-15

PRIOR PILING DATE: 1998-09-11

PRIOR PILING DATE: 1998-10-14

PRIOR PILING DATE: 1998-10-14

PRIOR PILING DATE: 1999-10-30

PRIOR FILING DATE: 1999-10-30

SEQ ID NOS: 26

LENGTHER OF SEQ ID NOS: 26
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Sequence 2, Application US/10851337

Publication No. US2004022932A1

GENERAL INFORMATION:
APPLICANT: NAGASAKI, Hiroaki
APPLICANT: NAGASKI, Hiroaki
APPLICANT: KATAOKA, Jiro
APPLICANT: KATAOKA, Jiro
APPLICANT: KATAOKA, Jiro
APPLICANT: KITAMOTO, Katsuhiko
ITILE OF INVENTION: Producing It
FILE REFERENCE: 199438US-8222-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/851,337

CURRENT FILING DATE: 2002-10-05-24

PRIOR APPLICATION NUMBER: US/10/262,083

PRIOR APPLICATION NUMBER: US/10/10-15

PRIOR APPLICATION NUMBER: US/10/10-15
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                                         Length 690;
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                               Query Match 100.0%; Score 29; DB 14; Length 6. Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Aspergillus oryzae US-10-262-083-18
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59; Search time 6.95312 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-10 29 Title: Perfect score: Sequence:

1 TYAMH S

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	. ;	Query		8	SUMMARIES	
. Po	Score	Match	Length	8	ID	Description
а	29	100.0	122	Н	M3HUGA	Iq heavy chain V-I
0	29	100.0	138	~	A35676	heavy chain
m	59	100.0	196	~	D71184	nvlate kinas
4	53	100.0	249	~	B83290	
Ŋ	29	100.0	1151	~	H71347	hypothetical prote
9	29	ö	1377	7	154632	, '
7	56		95	~	T34500	hypothetical profe
œ	56	89.7	196	~	IS0675	÷
Q	56	89.7	213	~	H86403	hypothetical profe
10	56	89.7	222	7	E90215	conserved hypothet
11	56	89.7	228	~	T22924	hypothetical profe
12	26	89.7	242	N	AD1165	R gubtilia vana n
13	26	89.7	242	N	AD1524	Subtilia Vvn
14	56	89.7	501	~	A29487	vtochrome B
15	56	89.7	501	~	A34236	D450
16	56	89.7	502	-	A34101	D450
17	26	89.7	504	8	A25222	0450
18	26	89.7	609	7	E82423	מיני ל
19	56		723	7	A84425	
20	56	89.7	801	~	B64679	α
21	56	89.7	852	-	GNLJGA	
22	56		852	ч	GNLJGB	pol polyprotein -
23	56	89.7	852	N	S29358	nol profein - borri
24	56	89.7	996	~	S18955	fix23-3 protein
25	26	89.7	1265	~	F84517	probable belieses
56	56	89.7	1385	~	T21706	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓
27	56	89.7	1506	~	T30886	intermentant proce
28	56	o	6260	~	T30228	polybotido cimthos
29	25		35	N	S26887	To heary chain y r
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Ig heavy chain V r Ig heavy chain V-I Ig heavy chain V-I Ig heavy chain V r	
\$46473 PL0120 \$17609 \$10385 \$26886 \$226886 \$229546 \$53076 PH1665 PH1644 PH1644 PH1646 PH1646 PH1666 B33936 PH1667	
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33 945 947 1008 1009 1111 1113 1113 1144	
00000000000000000000000000000000000000	
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ALIGNMENTS

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ö Indele .. 0 Mismatches ö 5; Conservative Matches

1 TYAMH 5 ||||| 31 TYAMH 35

RESULT 2
A35676
Ig heavy chain precursor V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999
C;Accession: A35676
R;White, M.B.; Word, C.J.; Humphries, C.G.; Blattner, F.R.; Tucker, P.W.
Mol. Cell. Biol. 10, 3690-3699, 1990
A;Title: Immunoglobulin D switching can occur through homologous recombination in human E A;Reference number: A35676; MUID:90287160; PMID:2113175
A;Accession: A35676
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Koss-references: GB:M38066; NID:g185466; PIDN:AAA52974.1; PID:g553407
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology < IMM>

||||| 50 TYAMH 54

1 TYAMH 5

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hypothetical protein TP0245 - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C; Accession: H7134,
Norris, Norris, Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinr 1800, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDorthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998 sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID:98332770; PMID:9665876
A; Status: Preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-1151 COLD.
A; Cross-references: UNIPROY: OB3273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AAC65235; Conseriental source: strain Nichols
C; Genetics: HOND.
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hypothetical protein ZK1248.17 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34500
B;Latrellle, P.
Submitted to the EMBL Data Library, June 1995
A;Pescription: The sequence of C. elegans cosmid ZK1248.
A;Resicutes number: Z21534
A;Resicutes: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T34500
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-95 zLAT
A;Cross_references: UNIPROT:023428; EMBL:U29244; PIDN:AAC71098.1; GSPDB:GN00020; CESP:ZKJ
A;Experimental source: strain Bristol N2; clone ZK1248
C;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 154632
Exprovence, D.L.; Curtiss, R.
Infect. Immun. 62, 1369-1380, 1994
A;Title: Isolation and characterization of a gene involved in hemagglutination by an avis
A;Reference number: I54632; MUID:94178945; PMID:8132344
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosacule type: DNA
A;Cross-references: UNIPROT:047692; GB:L27423; NID:g469235; PIDN:AAA24698.1; PID:g469236
C;Superfamily: IgA-specific metalloendopeptidase
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100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indele C
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C;Superfamily: syphilis spirochete hypothetical protein TP0245
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Nature 4066, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A; Reference number: A82950; MUID:2043737; PMID:10984043
A; Accession: B83290
A; Status preliminary
A; Mesidues: 1-249 cSTO>
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A;Status: preliminary, nucleic acid sequence not shown; translation not shown
A;Status: preliminary, nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Rosidues: 1-196 «KAW>
A;Cross-references: UNIPROT:059443; GB:AP000007; NID:g3236134; PIDN:BAA30867.1; PID:g325
A;Cross-references: Universe strain OT3
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: UNIPROT: Q9HZZ6; GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AAG0623
A, Experimental source: strain PAOl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenylate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: D71184
R;Accession: D71184
R; Kawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S; Sekin
B; Ohluku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi
DNA Res; S-76, 1998
A;Fitle: Complete sequence and gene organization of the genome of a hyper-thermophilic a
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                                                                           Query Match 100.0%; Score 29; DB 2; Length 138; Best Local Similarity 100.0%; Pred. No. 9; Matches 5; Conservative 0; Mismatches 0; Indels
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Query Match Best Local Similarity 100.. Best Local Si Conservative

157 TYAMH 161

8

1 TYAMH 5

Query Match 100. Best Local Similarity 100. Matches 5; Conservative

192 TYAMH 196

RESULT 5 H71347

1 TYAMH 5

C,Genetics: A,Gene: PH1753 C,Keywords: phosphotransferase

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S007 BI:85:9T C
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Fishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, Rad, Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A.; Description: Sulfolobus solfataricus complete genome.
A.; Reference number: A99139
A.; Accession: B90215
A.; Status: preliminary
A.; Molecule type: DNA
A.; Residues: 1-222 < KUR>
A.; Residues: 1-222 < KUR>
A.; Residues: 1-222 < KUR>
A.; Coss-references: UNIPROT: Q9UX67; GB: AEO06641; NID: g13813846; PIDN: AAK40980.1; GSPDB: GR
C.; Superfamily: hypothetical protein MJ0570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F58E6.8 - Caenorhabditis elegans
C.Species: T2994
R.McMurray, A.
Submitted to the EMBL Data Library, April 1996
A.Recession: T2294
A.Recession: T2294
A.Status: preliminary, translated from GB/EMBL/DDBJ
A.Rolecule Type: DNA
A.Residues: 1-228 < WIL.
A.Residues: 1-228 < WIL.
A.Residues: UNIPROT: Q20984; EMBL: Z70754; PIDN: CAA94778.1; GSPDB: GN00023; CESP: F56
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                                                                                                                                                                                                                                                                 conserved hypothetical protein [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #sequence_revision 24-May-2001 #cext_change 09-Jul-2004 C;Accession: E90215
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C,Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2
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Pred. No. 76;
1; Mismatches
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Best Local Similarity 80.0%;
Matches 4; Conservative 1
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202 TYALH 206
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14 TYALH 18
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177 TYALH 181
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A;Gene: CESP:F58E6.8
A;Map position: 5
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-196 < vIE>
A;Cross-references: UNIPROT:P41263; EMBL:X77960; NID:g457778; PIDN:CAA54922.1; PID:g4577
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Keference and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H86403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retinol-binding protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50675; S42887
R;Vielra, A.V.; Kuchler, K.; Schneider, W.J.
DNA Cell Biol. 14, 403-410, 1995
A;Title: Retinol in avian cogenesis: molecular properties of the carrier protein.
A;Reference number: I50675; MUID:95267350; PMID:7748490
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                     Query Match

89.7%; Score 26; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;36-195/Domain: lipocalin homology <LIP>
F;25-181,91-195,141-150/Disulfide bonds: #status predicted
A; Map position: 2
C; Superfamily: Caenorhabditis elegans major sperm protein
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Best Local Similarity 80.0.
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A Molecule type: DNA
A, Residues: 1-213 <STO>
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12 TYSMH 16
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396 TYALH 400
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               C;Genetics
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: Loua
A;Mosidues: 1-24 <GLA>
A;Mosidues: 1-24 <GLA>
A;Cross-references: UNIPROT:Q92DTO; GB:AL592022; PIDN:CAC95964.1; PID:g16413184; GSPDB:G
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Datesiphor: AD1524
C;Datesiphor: AD1524
C;Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.; Bloecker, F.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mayathors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AD1165

A;Accession: 
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80.0%; Pred. No. 83;
iive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Experimental gource: strain EGD-e
C.Genetics:
A.Gene: lmc0724
C.Superfamily: Bacillus subtilis hypothetical protein yvp8
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80.0%; Pred. No. 83;
ative 1; Mismatches
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Matches 4; Conservative
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Oylochrome P450 3A6 (version 1) - rabbit
NyAlternate names: cytochrome P450 3c
NyContains: oxidoreductase (EC 1.-.-.)
NyContains: oxidoreductase (EC 1.-.-.)
NyContains: oxidoreductase (EC 1.-.-.)
NyCocession: A29487
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Date: 31-Dec-1988 #sequence of cytochrome P450 3c cDNA and presence of two mRNA species NA;Reference number: A29487
A;Reference number: A29487
A;Reference number: A29487
A;Residues: 1-501 cDNA
A;Residues: 1-501 cD

RESULT 14

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Cytochrome P450 3A6 (version 2) - rabbit

NyAlternate names: cytochrome P450 3c

NyContains: oxidoreductase (EC.1.....)

Species oxidoreductase (EC.1.....)

Cypecies 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

CyAccession: A34236

RyPotenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;

J. Biol. Chem. 264, 16222-16228, 1989

A,Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and A; Reference number: A34236; MUID:89380226; PMID:2777787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-501 <POT>
A;Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
C;Genetics:
A;Gene: CYP3A6
A, Gene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygename;
F;301-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                                                                                                                                         Query Match 89.7%; Score 26; DB 2; Length 501; Best Local Similarity 80.0%; Pred. No. 1.7e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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OM protein - protein search, using sw model Run on:

October 14, 2005, 15:51:44; Search time 33.2812 Seconds (without alignments) 76.932 Million cell updates/sec

US-10-614-959-10 29 1 TYAMH 5 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Ö	homo s	xant	-	O9hzz6 pseudomonas		Q6n097 homo sapien	homo	Q83wr9 escherichia						083273 treponema p	O88093 escherichia	Q47692 escherichia	Q6jhn6 saccharopol			Q6xnp8 hevea brasi			Q66bk2 yersinia ps	Q86skl homo sapien	Q61mv3 photobacter		_	pasteu		_
		Δī	Q8RZ81	HV3H HUMAN	Q8PKV7	KADA PYRHO	9 <u>Z</u> ZH6O	Q962C9	Q6N097	Q68CN4	Q83WR9	Q6AQ19	Q9V6J4	Q9HGS1	6XAD6Ö	V222 FOWPV	Y245_TREPA	088093	047692	96ЛНИ6	Q62XJ3	Q23428	Q6XNP8	QBZZAS	072447	Q66BK2	Q86SK1	Q6LMV3	Q67RR8	RETB CHICK	Q9CKQS	Q9C6N1	Q9DG60
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de	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0	89.7	89.7	89.7	89.7	89.7	89.7	89.7		89.7		89.7		
		Score	29		29				29	29		. 29	29	29	53	29	29	29	29	59		26				26		56	56	56	56	56	26
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Q9ux67 sulfolobus Q20984 caenorhabdi Q88hp4 trichoderma Q8y918 listeria mo Q92dt0 listeria mo Q92dt0 listeria mo Q72zh3 listeria mo Q8wrc3 tetrahymena Q88sr2 pseudomonas Q7q8w1 anopheles g Q7qsw1 anopheles g Q6555 bacillus li Q65515 bacillus li Q65151k1 bacillus ce Q731k1 bacillus ce
09UX67 020984 085HP4 085HP4 081918 0922P10 0722H3 080MC3 080MC3 080MC3 080MC3 080MC3 080MC3 080MC3 080MC3 080MC3 081812
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# ALIGNMENTS

7. 1  OBEZBI OBEZBI OBEZBI OBEZBI OBEZBI OBEZBI OBEZBI OBEZBI OL-JUN-2002 (TrEMBLrel. 21, Created) OL-JUN-2002 (TrEMBLrel. 21, Last sequence update) OL-JUN-2002 (TrEMBLrel. 22, Last annotation update) BIO65G12.14 protein. Name=BIO65G2.14 protein. Subaryota; Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Elhhartoideae; Oryzeae; Oryzeae; Oryzea. NCBL_TaxID=39947;	DI=10.  TO T., Cheng  The Anna M., IT., The Anna M., The	AP003191; BAB90532.1; he; QBRZB1; -7677 MW; 6A936BD674BE00A3 CRC64; hc: T2 AA; 7677 MW; 6A936BD674BE00A3 CRC64; hc: T2 AA; 7677 MW; 6A936BD674BE00A3 CRC64; hc: T2 AA; 7677 MW; 6A936BD674BE00A3 CRC64; hc: T3 Minimatche	AN STANDARD; PRT; 122 AA. 1866 (Rel. 01, Created) 186 (Rel. 01, Last sequence update) 1004 (Rel. 44, Last annotation update) 186 (Chain V-III region GA.
LT 1  08RZ81  08.RZ81;  01UN-2002 (TrEM 01UN-2002 (TrEM 01CTT-2002 (TrEM 01CTT-20	SEQUENCE FROM N.A. Pubbmed=12447438; DN Saski T., Matasumol Wu J., Nilmura Y., Hosokawa S., Masuk Okamoto M., Ando T Hishita S., Hond Hishita S., Hond Ikion M., Itoh S., Karasawa W., Katagi Machita K., Maeharr Machita K., Maeharr Nagasaki H., Nakasi Nagasaki H., Nakasi Namiki N., Nagishi Shimokawa T., Shom Waki K., Yamagata P Zhong H., Iwama H., Yano M., Jiang J., Yano M., Jiang J.,	18L; ramer SQUEN Mat Loce	2 JMAN 73H HUMA 21769; 1-JUL-19 5-JUL-20 3 heavy
RESULT 10 00 11 0 00 00 00 00 00 00 00 00 00 00	R	Ouery State of State	RESULT HV3H HV ID HV AC AC DI 21 DI 21 DI 08

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Nature 417:459-463(2002).
EMBL, AE011840, AAM36012.1; -.
IRROPLY. IPRO01412; IRNA.synt I.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
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Matches
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SENDANDE FROM N.C.

MEDLINE=22022145; PubMed=12024277; DOI=10.1038/417459a;

A Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Cicarelli R.M.B., Coutinho L.L., Cureino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Mayski C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira W.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

"Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
VCBI_TaxIb=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrrolidone carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AA; 13166 MW; 74E5B6959E84100A CRC64;
                                                                                                                                                                                                       macroglobulin.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02052; M3HUGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. SMART; PS0815; IGV; 1. Direct protein sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein XAC2050.
                                                                                                                                                                                                                                                                                                                  HSSP, P01772; 2PB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig-like.
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les 5; Conserv
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                                                                          NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sakine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohiuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
Masuchi Y., Shizuya H., Kikuchi H.,
Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res 5:55-76(1988).

--- CATALYIC ACTIVITY: ATP + AMP = 2 ADP.
--- CATALYIC ACTIVITY: ATP + AMP = 2 ADP.
--- SUBCELLUJAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the archaeal adenylate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                   2; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 48, Last sequence update)
Adenylate kinaee (EC 2.7 4.3) (ATP-AMP transphosphorylase)
Name-adkA, OrderedLocusNames=PH1753;
Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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196 AA; 22413 MW; 26C834A1BE944D5F CRC64;
                              158 AA; 17289 MW; CIBIFB23AA6E930B CRC64;
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                                                                                   100.0%; Score 29; DB
100.0%; Pred. No. 42;
:ive 0; Mismatches
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Matches 5; Conservative
                                                                                                                 Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P43410; 1KI9.
Complete proteome.
SEQUENCE 158 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 TYAMH 161
                                                                                                                                                                                                                                                                     132 TYAMH 136
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                                                                                                                                                                                                           1 TYAMH 5
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059443;
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                                                                                         Query Match
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2007 ST:85:9T C
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Pseudomonas aeruginosa. Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadacee; Pseudomonas. VCBI_TaxID=287; 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PA2847; 249 AA PRT; PRELIMINARY; 

ö 100.0%; Score 29; DB 2; Length 249; 100.0%; Pred. No. 67; 0; Indels ive 0; Mismatches 0; Indels Local Similarity 100. Query Match Best Loc Matches

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01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Transcription factor Cnox4-Pc. PRELIMINARY; Q962C9 Q962C9; RESULT 6
Q962C9
AC Q962C9
DT Q1-D
DT O1-D
DT O1-D
DT O1-D
DT O1-M
DE PORO
OC EUKA
OC HYGE
OC HYGE
OC EUKA
I 1 CON
RRY YANEDL
DR HASSE
DR HASSE
DR HASSE
DR HASSE
DR INTE
DR FRIR
DR PRIR
DR PRIR

356 AA

Podocoryne carnea.
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydractiniidae, Podocoryne.

SEQUENCE FROM N.A.
MEDLINE=21349874; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
Yanze N., Spring J., Schmidli C., Schmid V.;
"Conservation of Hox/ParaHox-related genes in the early development a cnidarian.";

Dev. Biol. 236:38-98(2001).

-1- SUBCELLULAR LOCATION: Nuclear (By similarity).

EMBL; AV036693; AAK63185.1; -.

HSSP; P09089; IKZ2.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005700; F:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeodomain like.

InterPro; IPR009675; HTH lambrepressr.

Ffam; PP00064; HGMEODOX; I.

PRINTS; PRO0014; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6BB CRC64; SKE

ö Query Match
100.0%; Score 29; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels

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Gaps

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481 AA. PRT; PRELIMINARY; Q6N097

G6N097;
05-JUL-2004 (TERMELRE1. 27, Created)
05-JUL-2004 (TERMELRE1. 27, Last sequence update)
05-JUL-2004 (TERMELRE1. 27, Last sequence update)
05-JUL-2004 (TERMELRE1. 27, Last annotation update)
Hypothetical protein DKFZp686H20196.
Home sapiens (Human).
Hypothetical protein DKFZp686H20196.
Home sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A.

TISSUE-Human esophagus tumor;
G THE German Human coDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
A Pobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
R RSB; P0186.1: 1ADQ.
R RSB; P0186.1: 1ADQ.
R InterPro; IPR003109; IG.
R InterPro; IPR003109; IG.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R SWART; SM00409; IG. 2.
R SWART; SM00406; IGV: 1.
R SWART; SM00406; IGV: 1.
R SWART; SM00406; IGV: 1.
R RRSITE; PS00290; IG_MHC: UNKNOWN_2.

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RESULT 7

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Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels PROJECT CONTROLLE STATES WW, 47220D9E64BDF9BB CRC64; SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF9BB CRC64;

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Gaps

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50 TYAMH 54 1 TYAMH S

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RESULT 8
968CN4
1D 068CG
AC 068CG
DT 25-00
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DE HYPOI
GN Name:
OC BUKA:
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OGBCN4

OGBCN4;

OGBCN4;

25-CCT-2004 (TrEMBLrel. 28, Created)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
Hyporthetical protein DKFZp686E23209 (Fragment).
Name=DKFZp686E23209;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

SEQUENCE FROM N.A.

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25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Probable acetyl-coenzyme A synthetase. Name-acs; OrderedLocusNames=DP0825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00154; AMPBINDING.
PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                           [1]
SEQUENCE FROM N.A.
STRAIN=LSv54 / DSM 12343;
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                                         A Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., A Bloccker H., Boecher M., Wiemann S.;

Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

EMBL: CR79861; CR418705.1; -.

R EMBL: CR79861; CR418705.1; -.

R InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R Pfam; PF0764; G1-set; 3.

R Pfam; PF0764; G1-set; 3.

R SMART; SM00409; IG. 2.

SMART; SM00409; IG. 2.

R SMART; SM00406; IG. 1.

R PROSITE; PS50835; IG LIKE; 4.

R PROSITE; PS50835; IG LIKE; 4.
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Enterobacteriaceae; Escherichia.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY280856; AAP33781.1; -.

GO; GO:0004252; F:serine-type endopeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR009003; Peptidase_S6.

InterPro; IPR009003; Pept_Ser_Cys.

R Pfam; PF02935; IGAl; 1.

R PRINTS; PR00921; IGASERPTASE.

I NON TER 531 AA; 56485 WW; 60AC4E859A7AFC03 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 29; DB 2; Length 531; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 493 AA; S4117 MW; A1E4F5ED3FA8AB40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Tsh parcheln (Fragment).
Escherichia coli.
                                  The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 5; Conservative
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Q6AQ19;
25-OCT-2004 (
25-OCT-2004 (
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RESULT 9

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1083 with the control of the control

(TrEMBLrel. 28, Created) (TrEMBLrel. 28, Last sequence update)

RESULT 10

Q6AQ19 ID Q6 AC Q6 DT 25 DT 25

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hookkins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Asbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.W., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,
RA Durbins R.J., Bengelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fooler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                      Pubmeda1533914;
Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
Rabus R., Ruepp A., Frickey T., Rattei T., Amann J., Gellner K.,
Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.;
Klenk H.-P.;
From per C. Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
Environ. Macrobiol. 6:887-902(2004).
--- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Desulfotalea psychrophila:
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
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01-077-2002 (TrEMBLrel. 13, Created)
01-077-2002 (TrEMBLrel. 22, Last sequence update)
25-077-2004 (TrEMBLrel. 28, Last annotation update)
03915-PB (041270319)
Name-Drl-2; ORRNames-CG3915;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 29; DB 2; Length 544; 100.0%; Pred. No. 1.5e+02; rive 0; Mismatches 0; Indels
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
Interpro; IPR00873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

Jalali M., Kalueh F., Karpen G.H., Ke Z., Kennison J.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kernison J.A.,

Liu X., Mattei B., McIncosh T.C., Molecod M.P., McPherson D.,

Liu X., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.E.,

Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Nelson D.K., Nelson K., Saunders R.D., Scheeler F., Shen H.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

Spier E., Stden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Nalliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Alliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Alliams S.M., Woodager, Worley K.C., Zhu S., Zhu X., Smith H.O.,

Albbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-21426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Feiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Wan K., Gibbs R.A., Rubin G.G., Venter E.Inishing a whole-genome shotgun: Release 3 of the Drosophila Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE-22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Gaps

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Length 648;

100.0%; Score 29; DB 2; Length 6; 100.0%; Pred. No. 1.88+02; 1.1ve 0; Mismatches 0; Indels

Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative

R EMBL; AE003820; AAF58429.3; -.
R HSSP; PO8581; 1RIW.
R HSSP; PO8581; 1RIW.
R PLYBase; FEGN003791; Dr1-2.
R GO; GO:0004713; F:ATP binding; IEA.
GO; GO:0004713; F:ATP binding; IEA.
GO; GO:0004713; F:Drotein-tyrosine kinase activity; IEA.
GO; GO:0004740; F:transferase activity; IEA.
GO; GO:0004740; F:transferase activity; IEA.
R GO; GO:0004740; F:transferase activity; IEA.
R InterPro; IPR011009; Kinase.
R InterPro; IPR001245; Tyr_Dkinase.
R InterPro; IPR001245; Tyr_Dkinase.
R InterPro; IPR00306; Tyr_Dkinase.
R InterPro; IPR00306; WIF:
R PRINTS; PR001109; PROTEIN KINASE DOM; I.
R PROSITE; PS50011; PROTEIN KINASE DOM; I.
R PROSITE; PS50011; MIF; 1.
R RINGS: Transferase; Tyrosine-protein kinase.
SEQUENCE 648 AA; 71139 WW; 1B4FAA60CB84E457 CRC64;

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O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Glutaminase (EC 3.5.1.2).
Aspergillus oryzae.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TAXID=5062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thammarongtham C., Turner G., Moir A.J., Tanticharoen Cheevadhanarak S.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ database EMBL, AXO05477; AAG02575 1; GO; GO:0004359; F:glutaminase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 AA; 76226 MW; 6546BE2499D8D43C CRC64;
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Last sequence update)
Last annotation update)
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Q9UVX9;
01-MAY-2000 (TrEMBLrel. 13, Li
01-MAY-2000 (TrEMBLrel. 13, Li
01-DEC-2001 (TrEMBLrel. 19, Li
Glutaminase A.
Name=gtaA;
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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56 TYAMH 60
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1 TYAMH 5
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                                                                                                                                                                            RESULT 12
094631
1D 09463
AC 09463
AC 09463
DT 01-MA
DT 0
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Matches
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Q9UVX9
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STRAIN-Berkeley, Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

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                                                                    STRAIN-RIB40;
MEDLINE-20406523; PubMed=10952006;
MEDLINE-20406523; PubMed=10952006;
Kolbuchi K., Magasaki H., Yusaa A., Kataoka J., Kitamoto K.;
Kolbuchi K., Magasaki H., Yusaa A., Kataoka J., Kitamoto K.;
"Molecular cloning and characterization of a gene encoding glutaminase from Aspergillus oryzae.";
Appl. Microbiol. Biotechnol. 54:59-68(2000).
EMBL; AB029552; BAA86934.1; -.
SEQUENCE 690 AA; 76164 MW; E3D0B17841EEA00D CRC64;
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                      Fowlpox virus (FPV).
Viruses; delnA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.
NCBI_TaxID=10261;
Eukaryota, Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

BEDLINE-20193820.

DOI=10.1128/JV1.74.8.3815-3831.2000;

Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;

"The genome of fowlpox virus.";

J. VALCI. 74:3815-3831(2000).

-I. SIMILARITY: Contains 14 ANK repeats.
                                                                                                                                                                                                ö
                                                                                                                                                                      100.0%; Score 29; DB 2; Length 690; 100.0%; Pred. No. 1.98+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             093513;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name=FPV222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00248; ANK; 15.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50089; ANK_REPEAT; 7.
ANK repeat; Hypothetical protein; Repeat.
REPEAT
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ANK 4.
ANK 5.
ANK 6.
ANK 6.
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InterPro; IPR002110; ANK.
InterPro; IPR01810; F-box.
Pfam; PF00023; Ank; 13.
Pfam; PF00646; F-box; 1.
PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                     Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       423 TYAMH 427
                                                                                                                                                                                                                        1 TYAMH 5
                                                                                                                                                                                                                                                                                                     V222_FOWPV
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V222_FOWPV
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                                                                                                                                                                                                                                                                            Gaps
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1D Y245 TREPA

AC 083273;
DT 16-0CT-2001 (Rel. 40, Created)
DT 16-0CT-2004 (Rel. 40, Last sequence update)
DT 25-0CT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0245.
DS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                Match 100.0%; Score 29; DB 1; Length 747; Local Similarity 100.0%; Pred. No. 2.1e+02; es 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome, Hypothetical protein.
SEQUENCE 1151 AA, 127556 MM, EDB6353C32CB4056 CRC64;
ANK 9.
ANK 10.
ANK 11.
ANK 11.
ANK 12.
ANK 13.
ANK 13.
ANK 14.
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                                                                                                                                                                        85303 MW;
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     361 3
397 4
430 4
464 4
495 5
529 5
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us-10-614-959-11.rag

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version	- 2005
GenCore	(c) 1993
	Copyright

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October 14, 2005, 15:51:19; Search time 130.688 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-11 88 1 IISYDGSKKYYADSVKG 17 Title: Perfect score:

Sequence:

Scoring table:

2105692 segs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp200s:*
4: geneseqp200s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003s:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aav79069 Anti-fact			Human	Human	Single	Ada95732 Single ch	Single		Singl			-				Aay79076 Anti-fact	_		Human	1 Human	Human	Single	Human a	Plasm
0	AAY79069	ABB07230	2	ABP44905	ABP44903	ADG95730	ADG95732	0	ABP45103	ADG95930	0	ABB07186	ABO33850	ABO33836	ABB07169	ADI26654		ADP22108	ADE28443	ADD28233 p	ADD28321	ABP45679 P	ADG96506		ABB06275 P
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Query Match	100.0	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	7.76	96.6	95.5	95.5	95.5	95.5	94.3	94.3	94.3	94.3	•	94.3	94.3	94.3	94.3
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Result No.	-	8	Э	4	ß	9	7	<b>8</b> 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Aar76976 HSV-neutr Aar76976 HSV-neutr Abu56817 BONT/A HC Abu56866 BONT/A HC Aaw62799 Amino aci Aab40127 Anti-hIL1
AAN90298 AAY79078 AAY79078 AAN779078 AAN1732094 ADH89402 ADS23370 ADS52370 ADS52340 ADS52348 ADS82388 ADS82388 ADS82388 ADS82388	AAR (
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## ALIGNMENTS

Ź AAY79069 standard, peptide, 17

12-JUN-2000 (first entry)

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome, ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence

Homo sapiens.

WO200012562-A1.

39-MAR-2000

99WO-US019453. 26-AUG-1999;

28-AUG-1998;

98US-0098233P. 99US-0122767P. 03-MAR-1999;

(GETH ) GENENTECH INC.

Kirchhofer D; Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S; 

"PI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXA a vitamin K dependent plasma serime procease that participates in the blood coapulation pathways. The Gla domain of factor IXa and its zymogen factor. IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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Novel human antibody which binds human interleukin (IL)-4 receptor and is capable of inhibiting IL-4 induced biological activity, functions as IL-4 antagonist and is useful for treating septic arthritis, scleroderma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a human antibody (an interleukin (IL)-4 antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of
the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, atterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
antiarthritic; dermatological; antiulcer; antinflammatory; cytostatic;
antisickling; immunosuppressive; tuberculostatic; ophthalmological;
antianemic; antithyroid.
                                                                                                                                                                                                                                                    Gaps
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50. .66
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                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                     Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-IL-4 receptor MAb 6-2 heavy chain variable region.
                                                                                                                                                                                                                       Score 88; DB 3; I
Pred. No. 3.2e-07;
                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               ABB07230 standard; protein; 118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 73; 85pp; English
                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                  1 IISYDGSKKYYADSVKG 17
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19-SEP-2000; 2000US-0065343.
15-FEB-2001; 2001US-00785934.
01-MAY-2001; 2001US-00847816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001; 2001WO-US017094
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
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99. .107
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N-PSDB; ABA94330.
                                                                                                                                                                                         Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                RESULT 2
ABB07230
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inhibiting an IL-4-induced biological activity. (I) is also useful for inhibiting both IL-4-induced biological activity and IL-13-induced in a human, and for treating septic arthritis in a human afflicted with septic arthritis. (I) is also used for treating conditions such as septic/reactive arthritis, dermatitis herpetiformis, conditions such as septic/reactive arthritis, dermatitis herpetiformis, urticata (septical) ulcers, gastric inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease, inflammation, bowel disease, other disorders of the digestive system in which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the gastrointestinal tract), conditions in which IL-4-induced barrier disorders of the digestive system in the graphical partier function in the lung or gastrointestinal tract), scleroderma, hypertrophic scarring, Whipple's disease, benign prostate complete and proper sickle cell disease, benign prostate traction, kawasaki disease, sickle cell disease or crisis. Churge. Strauss syndrome, drave's disease, pre-eclampsia, sjogen's syndrome, caucoimmune lymphoproliferative syndrome, autoimmune blastering complete also find use as adjuvante muscular disease), and myasthenia garvis (an autoimmune blistering consequence represents an autoimmune mascular disease). IL-4 and as a consequence represents an anti-IL-4 receptor monoclonal antibody which it response would be beneficial in treating or preventing the disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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Pred. No. 4.1e-06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6-2 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BLyS binding scFv SEQ ID 1323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP45312 standard; protein; 248 AA.
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2000US-0240816P.
2001US-0276248P.
2001US-0277379P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.9%;
94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 94.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118 AA;
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16-MAR-2001; 2
21-MAR-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP45312;
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This invention describes novel antibodies that immunospecifically bind to be Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell to proliferation and differentiation. The antibodies of the invention have proliferation, immunosuppressive, immunostimulant, immunomodulatory, antithematic and antihals activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumacoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and cautibodies and fragments of the antibodies described in the method of the invention
                                                           Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                      Claim 1; Page 1981-1982; 3148pp; English
          WPI; 2002-114799/15
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Gaps ö 98.9%; Score 87; DB 5; Length 248; 94.1%; Pred. No. 9.3e-06; arive 1; Mismatches 0; Indels Query Match
Best Local Similarity 94.1
Matches 16; Conservative Sequence 248 AA;

1 IISYDGSKKYYADSVKG 17

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ABP44905 standard; protein; 248 ABP44905;

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Human BLyS binding scFv SEQ ID 916.

19-AUG-2002 (first entry)

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulat; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome. 

Homo sapiens

WO200202641-A1.

10-JAN-2002

15-JUN-2001; 2001WO-US019110.

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P.

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

ä Hilbert F, Vaughan Choi GH, Barash SC, WPI; 2002-114799/15 Ruben SM,

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 1495-1496; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell control of the cumour necrosis factor (TNF) super family and induces B cell control of the invention and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antithemmatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant Expression of BLyS. They may also be associated with aberrant axpression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and iseases e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiancy (e.g. common variable immunodeficiency (c.UID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of

Sequence 248 AA;

Сарв ö 98.9%; Score 87; DB 5; Length 248; 94.1%; Pred. No. 9.3e-06; ive 1; Mismatches 0; Indels 16; Conservative Best Local Similarity Query Match Matches

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ABP44903 standard; protein; 248 AA.

fuman BLyS binding scFv SEQ ID 914.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunosetimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

10-JAN-2002.

15-JUN-2001; 2001WO-US019110. 

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Hilbert D;

RESULT 5 ABP44903

(first entry) 19-AUG-2002

Homo sapiens

VO200202641-A1.

16-JUN-2000, 2000US-0212210P. 17-CCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0273799. 25-MAY-2001; 2001US-0293499P.

Choi GH, Vaughan T, Barash SC, Ruben SM,

WPI; 2002-114799/15.

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell conformed differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant appression of BLyS. They may also be administered to treat diseases associated with aberrant and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ADDS)). ABP41728 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiathritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain antibody that immunospecifically binds BLyS SeqID 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.9%; Score 87; DB 5; Length 248; 94.1%; Pred. No. 9.3e-06; cive 1; Mismatches 0; Indels
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                                                                                                                  Claim 1; Page 1492-1493; 3148pp; English.
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19-DEC-2001; 2001US-0340817P.
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Matches 16; Conserv
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Gaps

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable composition to factor immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The composition, disquests and prognosis of diseases related to the ederection, diagnosis and prognosis of diseases related to the ederection, diagnosis and prognosis of diseases related to the caperrant expression or inappropriate function of BLyS or its receptor. As uch, these compositions are useful for identifying immune diseases concluding myserbania and rheumatoid arthritis, infectious diseases such disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and corivities such as anticheumatic, antiallergic and cytostatic. This collypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of directely from WIPO at ftp.wipo.int/published pot_sequences.
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Pred. No. 9.3e-06;
1; Mismatches 0; Indels
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19-DEC-2001; 2001US-0340817P.
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94.1%;
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 248 AA;
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Sequence 248 AA;

Gaps ; 0 98.9%; Score 87; DB 7; Length 248; 94.1%; Pred. No. 9.3e-06; Live 1; Mismatches 0; Indels Best Local Similarity 94.1 Matches 16; Conservative Query Match

99 1 IISYDGSKKKYYADSVKG 

ADG96139 standard; protein; 248 AA.

11-MAR-2004 (first entry)

Single chain antibody that immunospecifically binds BLyS SeqID 1323.

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; ALDS; leukaemia; carcinoma; lymphoma; atthriticheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic. 

Unidentified

WO2003055979-A2.

10-JUL-2003

14-NOV-2002; 2002WO-US036496

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Choi GH, Vaughan TJ, Hilbert D; Ruben SM, Barash SC,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

Example 1; SEQ ID NO 1323; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1343 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (GCFWs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monky BLyS. The cypesent invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of such antibodies in various methods for the detection, diagnosis and prognosis of identifying immune disorders including myasthenia gravis and multiple sclerosis inflammatory compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis inflammatory disorders including leukemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This continited sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the principle for the principle for the principle format and relevance of the principle. directely from WIPO at ftp.wipo.int/pub/published pct_sequences. 858888888888888888888888888888888

Sequence 248 AA;

Gaps ö ch 98.9%; Score 87; DB 7; Length 248; 1 Similarity 94.1%; Pred. No. 9.3e-06; 16; Conservative 1; Mismatches 0; Indele Local Similarity Best Loca Matches

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1 IISYDGSKKYYADSVKG 17 

ð 셤 RESULT 9 ABP45103

ABP45103 standard; protein; 251 AA.

(first entry) 19-AUG-2002 Human BLyS binding scFv SEQ ID 1114.

BLyB; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive, immunostimulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

MO200202641-A1.

10-JAN-2002.

15-JUN-2001; 2001WO-US019110.

16-JUN-2000, 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P. 

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Choi GH, Vaughan T, Barash SC, Ruben SM,

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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

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Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosais factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity and can be used in vaccines to inhibit the expression and activity of an antibodies bind to biological samples and may be used in this way to disgnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                              diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87; DB 5; Length 251;
Pred. No. 9.4e-06;
1; Mismatches 0; Indels
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diagnosis and treatment of cancers and immune disorders.
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                                     Claim 1; Page 1731-1732; 3148pp; English.
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19-DEC-2001; 2001US-0340817P.
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                   the invention
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Matches
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Gaps

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to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single cohain antibody molecules (scFvs) derived, preferably, from the variable cohain antibody molecules (scFvs) derived, preferably, from the variable composition to make the variable region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The contract special properties and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders such, these compositions are useful for identifying immune disorders uncluding mysathenia agravis and multiple sclerosis, inflammanory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and conjunctions and antiathering in an exhibiting various cartivities such as antitheumatic, antiallergic and cytostatic. This collypeptide sequence is a single chain antibody that binds BLyS of the cinvention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format confired the printed specification, but was obtained in electronic format.
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29-APR-2002; 2002US-0376408P.
27-SEP-2002; 2002US-0414053P.
25-NOV-2002; 2002US-0428807P.
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Nile virus

The present invention describes a human heterodimeric antibody (I) (fragment) having a binding affinity of at least lx10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has vincide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as antehrax, botulinum, smallpox, Venezuelan equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain of the present invention. Claim 11; SEQ ID NO 97; 67pp; English. 

Sequence 135 AA;

/ Match
135;
Local Similarity 94.1%; Pred. No. 6.8e-06;
les 16; Conservative 1; Mismatches 0; Indels 1 IISYDGSKKYYADSVKG 17 Query Match

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ABB07186 standard; protein; 119 AA.

ABB07186;

(first entry) 13-MAR-2002

sHigM22 heavy chain variable region clone B sequence.

Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.

WO200185797-A1.

15-NOV-2001

30-MAY-2000; 2000WO-US014902.

10-MAY-2000; 2000US-00568351

(MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

Rodriguez M, Miller DJ, Pease LR;

WPI; 2002-066596/09. N-PSDB; ABA94243.

Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis

Claim 23; Fig 17; 219pp; English.

The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (1) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting G22+ signaling with oligodendrocytes. An humanised antibody to (1) can be selected from antibody sHIGM22 (LYM 22), eVHIGM MSI19D10, ebv HIGM cB22bG8, AKGN4, CB21E12, CB21E7 or MSI19ES. (1) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in 

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a post-order of muan or domestic animal with a viral demyelinating disease, or a post-order of muan or domestic animal with a viral demyelinating disease, or a post-order of stamulating the proliferation of gial cells from mixed cell culture. (I) is also useful for stimulating remyelination of CNS axons. The antibodies care useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful concerned multiple sclerosis, Parkinson's disease, Alzheimer's clisease, amyortophic lateral sclerosis (ALS), a viral demyelinating clisease, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the sHigM22 heavy axy axy and a constructions acid sequence. 

Sequence 119 AA;

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Gaps ; 0

0; Gapa 96.6%; Score 85; DB 5; Length 119; 94.1%; Pred. No. 8.6e-06; ive 1; Mismatches 0; Indels Local Similarity 94.1 Query Match Best Loca Matches

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RESULT 13 ABO33850

ABO33850 standard; peptide; 17 AA.

(first entry) 18-SEP-2003

Anti-GPI-antibody heavy chain complementarity determining region #10.

Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide; anti-GPI-antibody; GPI; glucose-6-phosphate isomerase; autoimmune disease; rheumatoid arthritis; heavy chain variable region; VH; complementarity determining region; CDR.

US2002146753-A1.

10-OCT-2002.

06-APR-2001; 2001US-00828708.

06-APR-2001; 2001US-00828708. (BURT/) DITZEL H. (BURT/) BURTON D R. (SCHA/) SCHALLER M. 

Schaller M; Burton DR, Ditzel H,

WPI; 2003-521517/49.

Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.

Claim 3; Fig 4A; 47pp; English.

The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods a compositions are used for disgnosis and treatment of human autoimmune disease, e.g., human rheumstoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region

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Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious
                                                              Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                          sHigM22 heavy chain variable region clone A sequence
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                     (first entry)
                                                                                                                                                                                                                                                        Miller DJ,
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                                                                                                                                                                                                                                                                                            N-PSDB; ABA94216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.
                                                                                                                                                                                                                                                                                   anti-GPI-antibody, GPI; glucose-6-phosphate isomerase; autoimmune disease; rheumatoid arthritis; heavy chain variable region;
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                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.5%; Score 84; DB 7; Length 112; 88.2%; Pred. No. 1.2e-05; ive 2; Mismatches 0; Indels
                                              Score 84; DB 7; Length 17;
Pred. No. 1.4e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Human anti-GPI-antibody heavy chain variable region #3
                                                                                                                                                                              AB033836 standard; protein; 112 AA
    complementarity determining region
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                                                Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
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(SCHA/) SCHALLER M.
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Pease LR;

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The invention provides a neuromodulatory agent (I) capable of promoting central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of inducing remyelination, central nervous system (CNS). (I) is capable of antibody to (I) can be signaling with oligodendrocytes. An humanised antibody to (I) can be capable of building melipoly, every High Melipoly. (I) can be considered antibody aliga22 (LMM 22), ebvHigh Melipoly. (I) can be selected from antibody shiga22 (LMM 22), ebvHigh Melipoly. (I) is useful for stimulating consideration of CNS axons, or treating demyelinating proliferation of glial cells in consideration of customers and cells in memman in need considerating the preferably useful for treating a demyelinating disease of CNS (CNS). (I) is preferably useful for treating a human being having multiple sclerosis, or a consume infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a post-neural disease of CNS. (I) is also useful for simulating remyelination of CNS axons. The antibodies are useful for stimulating remyelination of CNS axons. The antibodies consumed the proliferation of gial cells from mixed cell culture. (I) is also useful for stimulating remyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful continued and other conditions in the CNS where nerves are consistent and other conditions in the CNS where nerves are conditions and the conditions in the CNS where nerves are conditions and the conditions in the CNS where nerves are conditions and the conditions in the CNS where nerves are conditions and the conditions
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88.2%; Pred. No. 1.3e-05;
iive 2; Mismatches 0;
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ABB07169 standard; protein; 119 AA.

RESULT 15 ABB07169 ID ABBC

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Conservative

Matches

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-211-202-141

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US-08-311-3978-46

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Gapop 10.0 , Gapext 0.5
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Sequence 102, App
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Sequence 11, Appl
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Sequence 2, Appl
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100.0%; Score 88; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adams, Camelia W.
APPLICANT: Adams, Camelia W.
APPLICANT: Bevoux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L.
APPLICANT: Hulp E.
APPLICANT: Witchhofer, Daniel
APPLICANT: Sugget, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US 60/098,233
FARLIER PILING DATE: 1999-08-26
EARLIER PILING DATE: 1998-08-28
EARLIER PILING DATE: 1998-08-28
EARLIER PILING DATE: 1998-08-28
EARLIER PILING DATE: 1998-08-36
EARLIER PILING DATE: 1998-08-38
EARLIER PILING DATE: 1998-03-03
SEQ ID NO 11
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-383-667-18

Sequence 18, Application US/09383667

Sequence 18, Application US/09383667

GENERAL NO. 6624295

GENERAL THORMATION:

APPLICANT: Adams, Camelia W.

APPLICANT: Baton, Dan L.

APPLICANT: Hass, Philip E.

APPLICANT: Yirchhofer, Daniel

APPLICANT: Suggett, Abelley

TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies

FILE REFERENCE: P1661R2
US-09-456-090A-102
US-09-456-090A-108
US-09-455-091A-110
US-09-453-234-102
US-09-453-234-110
US-08-862-124-11
US-08-862-124-14
US-09-560-198A-12
US-09-560-198A-2
US-09-560-198A-2
US-09-560-198A-10
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
US-08-124-840B-22
                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-383-667-11
; Sequence 11, Application US/09383667
Patent No. 6624295
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IISYDGSKKYYADSVKG 17
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   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-11
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US-09-424-840B-36
US-09-424-840B-36
Sequence 36, Application US/09424840B
Fatent No. 6790938
FACENERAL INFORMATION:
APPLICANT: Beacht Cold, Peter
APPLICANT: Bacher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 10054-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
FRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
FRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
FRIOR OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
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is Sequence 95, Application US/09424840B
is Sequence 95, Application US/09424840B
is Patent No. 6790398
is GANERAL INFORMATION:
APPLICANT: Barcherold, Peter
intile De Invention: APPLICANT: Barcherold, Peter
intile De Invention: APPLICANT: Barcherold, Peter
intile De Invention: APPLICANTON: ANT-GPIIB/IIIA RECOMBINANT ANTIBODIES
intile REFERENCE: 100544-0949
intile Reference: 10954-0949
intile APPLICATION NUMBER: US/09/424,840B
intile APPLICATION NUMBER: DE 19820663.1
intile APPLICATION NUMBER: DE 1975527.7
intile APPLICATION NUMBER: DE 1972394.8
intile APPLICATION NUMBER: DE 1972396.66
intile APPLICATION NUMBER: DE 19752304.8
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88.2%; Pred. No. 1.2e-06;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 93.2%; Score 82; DB 4; Le 1 Similarity 100.0%; Pred. No. 1.2e-06; 16; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VISYDGSNKYYADSVKG 17
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Best Local Similarity 88.2
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 16; Conserv
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                                                                                                                                                                                                                                                                               LENGTH:
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Sequence 16, Application US/09383667

Patent No. 6624295

GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Beroux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Hass, Philip E.
APPLICANT: Hass, Philip E.
APPLICANT: Kirchnfer, Daniel
APPLICANT: Kirchnfer, Daniel
APPLICANT: Kirchnfer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENITON: Human Anti-Factor IX/IXA Antibodies
TILE REFERENCE: 91661R2
CURRENT APPLICATION NUMBER: US/09/383,667

CURRENT FILING DATE: 1998-08-28

EARLIER APPLICATION NUMBER: US 60/122,767

EARLIER FILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 16

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Patent No. 6624295

GENERAL INFORMATION:
APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Hass, Philip E.
APPLICANT: Judde, J. Kevin
APPLICANT: Suggett, Shelley
TILLE OF INVENITON: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2

CURRENT APPLICATION NUMBER: US/09/383,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 82; DB 4; Length 17; 88.2%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83; DB 4; Length 17;
Pred. No. 8.1e-07;
0; Mismatches 1; Indels
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                                                       CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 18
LENGTH: 17
                   CURRENT APPLICATION NUMBER: US/09/383,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲;
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-09-383-667-20
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US-09-424-840B-108
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Sequence 97, Application US/09424840B

GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR PPLICATION NUMBER: DE 19755227.7
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR PILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
LENGTH: 17
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; Batent No. 6790938
; GRNERAL INFORMATION:
APPLICANT: Berchtold, Peter
CURRENT APPLICATION NUMBER: US/09/424,840B
PRIOR FILING DATE: 1998-05-08
PRIOR FILING DATE: 1998-05-08
PRIOR PILING DATE: 1998-12-12
PRIOR APPLICATION NUMBER: DE 1975527.7
PRIOR APPLICATION NUMBER: DE 19753904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
LENGTH: 17
                                                                                                                                                                Ouery Match
93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels
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Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1.
                                                                                                                                                                                                                                                                                        1 IISYDGSKKYYADSVKG 17
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SOFTWARE: Patentin version 3.1
SEQ ID NO 95
LENGTH: 17
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                                                                                       ; ORGANISM: Homo sapiens
US-09-424-840B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-97
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ORGANISM: Homo sapiens
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US-09-424-840B-97
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                                                                        TYPE: PRT
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Gaps
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APPLICANT: BAIER, Michael
APPLICANT: BAIER, Michael
APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Combinatorial approach
NUMBER OF SEQUENCES: 144
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
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       Length 17;
                                                   1; Indels
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Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 23-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
  Score 82; DB 4; I
Pred. No. 1.2e-06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-58P-1992
CLASSIFTCATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-58P-1991
RIGR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-58P-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
RIGG APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG M. CLOUGH
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
                                                                                      1 IISYDGSKKYYADSVKG 17
                                                                                                                  1 VISYDGSNKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118:
Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Best Local Similarity
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APPLICANT: JESPERS, Laurent Coursell APPLICANT: WINTER, Gregory Paul TITLE OF INVENTION: Production of chimeric antibodies - a TITLE OF INVENTION: combinatorial approach TITLE OF INVENTION: combinatorial approach CORRESPONDENCE ADDRESS: 144
CORRESPONDENCE ADDRESS: ADDRESSE: Borun ADDRESSEE: Bor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER ERADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/211,202

FILING DATE: 23-SEP-1992

CLASSIFICATION NUMBER: GB 912025.3

FILING DATE: 32-SEP-1991

PRIOR APPLICATION NUMBER: GB 912037.8

FILING DATE: 25-SEP-1991

PRIOR APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206312.6

FILING DATE: 15-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: BCT/GB92/00883

FILING DATE: 15-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: DATA W. Clough

REFERENCE/DOKET NUMBER: 28111/31960

TELLCOMMUNICATION NUMBER: 28111/31960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 82; DB 1; Length 116; 88.2%; Pred. No. 8.7e-06; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Borun
STREET: 6310 Seare Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SO VISYDGSNKYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IISYDGSKKYYADSVKG
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312-474-0448
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Clackson, Timothy
APPLICANT: Minter, Timothy
APPLICANT: Monert, Timothy
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REPERENCE: 213839-00013
CURRENT APPLICANTON NUMBER: US/09/726,219A
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                                  Gaps
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Patent No. 5565312
GENERAL INFORMATION:
APPLICANT: HOGGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR PAPLICATION NUMBER: GB 9015198.6
PRIOR PLILNG DATE: 1990-10-19
PRIOR PLILNG DATE: 1991-03-06
PRIOR PLILNG DATE: 1991-03-06
PRIOR PLILNG DATE: 1991-03-16
PRIOR PLILNG DATE: 1991-07-10
PRIOR PLILNG DATE: 1993-01-08
PRIOR PLILNG DATE: 1993-01-08
PRIOR PLILNG DATE: 1993-01-08
PRIOR PLILNG DATE: 1993-01-08
PRIOR PLILNG DATE: 1991-07-10
PRIOR PLILNG DATE: 1993-01-08
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 167, Application US/09726219A Patent No. 6806079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson, Kevin
Hoogenboom, Hendricus
Griffiths, Andrew
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                                                                                                                                                                           SO VISYDGSNKYYADSVKG 66
                                                                                                                       1 IISYDGSKKYYADSVKG 17
                                          15; Conservative
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, ORGANISM: Homo sapiens
US-09-726-219A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-211-202-141
                                               Matches
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Sequence 115, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Hendo, Tasuku
APPLICANT: Matauda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
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us-10-614-959-11.rai
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FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER: TOM
REGISTATION NUMBER: 38,498
REGISTATION NUMBER: 38,498
REGISTATION NUMBER: 36,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-960
TELEPAX: (415) 543-960
TELEPAX: (415) 543-960
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94105-1492
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INCOMEDIATION

Sequence 46, Application US/08331398A

Patent No. 5608039

GENERAL INFORMATION:

APPLICANT: Pastan, Ira

APPLICANT: PatrGerald, David

APPLICANT: Brinkmann, Ulrich

APPLICANT: Single Chain B3 Antibody Fusion Proteins

ITLE OF INVENTION: and Their Uses (as amended)

CORRESPONDENCES.

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Plaza

CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 82; DB 3; Length 117;
88.2%; Pred. No. 8.8e-06;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IND FC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-CCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
                                                                                                                                                                                                       CURRENTING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows95
SOFTWARE: FASTSEQ for Windows95
SOFTWARE: FASTSEQ for Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: JO-MAY-1996
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNSY AGRAY INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
TYPE: amino acids
ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IISYDGSKKYYADSVKG 17
                                                                             STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.2°
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809A-115
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US-08-331-397B-46

Sequence 46, Application US/08331397B

Patent No. 5981726

Patent No. 5981726

Patent No. 5981726

APPLICANT: Pastan, Ira

APPLICANT: Pastan, Ira

APPLICANT: Pastan, Itai

TITLE OF INVENTION: Chimeric and Mutationally Stabilized TumorTITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Plaza

GITY: San Francisco

STATE: California ö Query Match 93.2%; Score 82; DB 1; Length 119; Best Local Similarity 88.2%; Pred. No. 8.9e-06; Matches 15; Conservative 1; Mismatches 1; Indels FEATURE:

LOCATION: 1..19

OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)" COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FLING DATE: US-OCT-1994
CLASSIFICATION NUMBER: US 07/767,331
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/56,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION: NAME: Hunter, Tom REGISTRATION NUMBER: 38,498 REPERENCE/DOCKET NUMBER: 015280-126120US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600

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Search completed: October 14, 2005, 16:22:00 Job time : 33.4688 secs
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Sequence 46, Application US/08759804A

Patent No. 599026

GENERAL INFORMATION:
APPLICANT: PitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Brinkmann, Ulrich
APPLICANT: PitzGerald, David J.
APPLICANT: Pai, Lee
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                   NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
GTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
US-08-331-3978-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIF: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
FRIOM APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 30-SEP-1991
FRIOM APPLICATION NUMBER: US 07/767,331
FILING DATE: 12-OCT-1990
ATTOMNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTOMNEY/AGENT INFORMATION:
ANAME: Webber Ellen L.
REGISTRATION NUMBER: 32,762
TELEPHONE: (415) 576-0200
INFORMATION FOR METATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR METATION:
SEQUENCE (415) 576-0300
INFORMATION FOR METATICS:
FENERAL (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 82; DB 2; I
88.2%; Pred. No. 8.9e-06;
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.29
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-759-804A-46
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps
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                                                                                                           /note= "Human fetal immunoglobulin
56Pl'CL Variable Heavy chain (V-H)"
                                                                                                                                                                                                                                                                       1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                    MAME/KEY: Procein
COCATION: 1.119
OTHER INFORMATION: 7
OTHER INFORMATION: 5
US-08-759-804A-46
STRANDEDNESS
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October 14, 2005, 16:20:10; Search time 120.859 Seconds (without alignments) 58.615 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUB_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1859788 seqs, 416717961 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                US-10-614-959-11
88
1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                           OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                Run on:
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Sequence 300, App Sequence 262, App Sequence 914, App Sequence 914, App Sequence 914, App Sequence 914, App Sequence 1323, Ap Sequence 1114, Ap Sequence 1114, Ap Description US-10-989-462-300 US-10-989-462-262 US-09-880-748-914 US-09-880-748-915 US-10-293-418-1323 US-10-293-418-1323 US-10-293-418-1323 US-10-293-418-1323 US-10-293-418-1313 US-10-293-418-1114 US-10-989-462-276 * Query Match Length DB Score 87 87 87 87 87 87 87 87

Sequence 97, Appl	9	4	4	2	e 10	6.7	e 14	28	11	6	7	99	97	Н	62	48	46	9	21	39	21	Sequence 81, Appl	36	95	97	70	23	11	21	39	2	81,	Sequence 47, Appl	
US-10-364-743-97	US-10-452-593-97	US-09-828-708-24	US-10-630-009-24	US-09-828-708-10	US-10-630-009-10	US-10-010-729-7	US-10-727-155-14	US-10-292-088-58	US-10-364-743-11	US-10-364-743-99	US-10-452-593-11	US-10-452-593-99	US-09-880-748-1690	1-293-418-16	0-292-088-6	9-972-656-4	384-060-4	US-10-399-701-6	1-396-578-2	US-10-396-578-39	1-396-578-5	US-10-396-578-81	7	-844-4	10-844-4	-	-864-01	-10-726-	11-074-	-11-074-	11-074-	US-11-074-803-81	0-269-	
	16		11		11									12	15	10	15	15	16	16	16	16	16	16	16	16	16	11	20	20	20	20	15	
135	135	17	17	101	101	119	123	125	137	137	137	137	252	252	470	17	17	17	17	17	17	11	17	17	17	17			17	17	17	17	41	
97.7	7.76	95.5	95.5	95.5	95.5	95.5	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	93.2	
86	96	84	84	84	84	84	83	83	83	83	83	83	83	83	83	85	82	85	83	85	82	85	82	82	82	82	82	82	82	82	82	85	83	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	. 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

#### ALIGNMENTS

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Gaps
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Sequence 300, Application US/10989462
| Publication No. US20050220795A1
| GENERAL INFORMATION:
| APPLICANT Witterup, K. Dane
| APPLICANT: Witterup, K. Dane
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: 01997-329001
| CURRENT APPLICATION WUMBER: US/10/989, 462
| CURRENT FILING DATE: 2004-11-15
| PRIOR FILING DATE: 2003-11-14
| PRIOR FILING DATE: 2004-04-19
| NUMBER OF SEQ ID NOS: 319
| SOFTWARE: FREESE 2004-04-19
| SOFTWARE: FREESE 2004-04-19
| SEQ ID NO 300
| LENGTH: 17
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98.9%; Score 87; DB 18; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IISYDGSKKYYADSVKG 17
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ORGANISM: Artificial Seguence
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1 VISYDGSKKYYADSVKG 17

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US-09-880-748-916
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Sequence 914, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5.3

CURRENT FILING DATE: 2001-06-15

PRIOR PLLICATION NUMBER: 05/240,816

PRIOR PLLICATION NUMBER: 60/240,816

PRIOR PLLING DATE: 2000-10-17

PRIOR PLLING DATE: 2001-03-16

PRIOR PLLING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 32-39

SEQ ID NO 914

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LEMMORT. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
     Sequence 252, Application US/10989462
Sequence 252, Application US/10989462
Sequence 252, Application No. US20050220795A1
GENERAL INFORMATION:
APPLICANT: Wittrup, X. Dane
APPLICANT: Wittrup, X. Dane
APPLICANT: Yeary YIK Andy
TITLE OF INVENTION: AMTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF;
FILE REFERENCE: 01997-329001
CURRENT APPLICATION NUMBER: US/0/989,462
CURRENT FILING DATE: 2004-11-15
PRIOR PLICATION NUMBER: US 60/520,114
PRIOR PLICATION NUMBER: US 60/520,114
PRIOR PLICATION NUMBER: US 60/53,514
PRIOR PLICATION NUMBER: US 60/53,514
PRIOR PLICATION NUMBER: US 60/53,514
PRIOR PLICATION NOW: 319
SOFTWARE: FESTEGO for Windows Version 4.0
SEQ ID NO 262
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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Best Local Similarity 94.11
Matches 16; Conservative
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, OKGANISM: Homo sapiens
US-09-880-748-914
US-10-989-462-262
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US-09-880-748-1323

Sequence 1323, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF53

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/215,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/214,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3239

SEQ ID NO 1323

LINGTH. 248
US-09-880-748-916
; Sequence 916, Application US/09880748
; Publication No. US20030059937A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT APPLICATION NUMBER: 60/212,210
FRIOR FILING DATE: 2000-66-15
; PRIOR FILING DATE: 2000-66-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PATCHTIN VUMBER: 60/293,499
; SUFTWARE: PATCHTIN VET. 2.0
; SEQ ID NO 916
; LENGTH: 248
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Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
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98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
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CORGANISM: Homo sapiens
US-09-880-748-1323
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Gaps

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Length 248;

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Sequence 13.3, Application US/10293418

Publication No. US20030223996A1

GENERAL INPORMATON:

AGENERAL INPORMATON:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPRENCES: PF23-P2

CURRENT PELICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/394,89

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-16

PRIOR FILING DATE: 2001-06-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2000-01-0-16

PRIOR PILING DATE: 2000-01-0-16

PRIOR PILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

**CHARLES OF SEQ ID NOS: 3247
                                                                                                                          Query Match 98.9%; Score 87; DB 15; Length 24 Best Local Similarity 94.1%; Pred. No. 2.5e-05; Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-293-418-916
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US-10-293-418-1323
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US-10-293-418-1323
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RESULT 6

US-10-293-418-914

i Sequence 314, Application US/10293418

i Publication No. US2003022396A1

i GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

CURRENT PILING DATE: 2002-11-27

PRIOR PPLICATION NUMBER: US/10/293,418

CURRENT PILING DATE: 2001-11-16

PRIOR PPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-12-19

PRIOR PLICATION NUMBER: 09/880,748

PRIOR PLICATION NUMBER: 09/880,748

PRIOR PLICATION NUMBER: 60/293,499

PRIOR PLICATION NUMBER: 60/293,499

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-06-25

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2000-06-16

PRIOR PLILING DATE: 2000-06-16
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Sequence 916, Application US/10293418

Sequence 916, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

PRIOR PLING DATE: 2002-11-27

PRIOR PLING DATE: 2001-11-16

PRIOR PLING DATE: 2001-12-19

PRIOR PLING DATE: 2001-12-19

PRIOR PLING DATE: 2001-16-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-31

PRIOR PLING DATE: 2001-05-31

PRIOR PLING DATE: 2001-05-36

PRIOR PLING DATE: 2001-05-16

PRIOR PLING DATE: 2000-06-16

PRIOR PLING DATE: 2001-05-34

PRIOR PLING DATE: 2000-06-16

PRIOR PLING DATE: 2000-06-16
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CORGANISM: Homo sapiens
US-10-293-418-914
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATON NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
98.9%; Score 87; DB 15; Length 248; 94.1%; Pred. No. 2.5e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                ; Sequence 1114, Application US/09880748; Publication No. US20030059937A1; GENERAL INFORMATION:
                                                                                                                                    1 IISYDGSKKYYADSVKG 17
Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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Gaps

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Query Match
97.7%; Score 86; DB 15; Length 135;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   Query Match 98.9%; Score 87; DB 18; Length 252; Best Local Similarity 94.1%; Pred. No. 2.5e-05; Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97, Application US/10364743
; Sequence 97, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Waruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
APPLICANT: No. US20040009178A1an, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT APPLICATION NUMBER: US 60/428,807
; RIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SGC ID NO 97
; LEGTH: 135
; TVPE: DOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Molan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REPREBRUCE: 98 CIP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-02-11
                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Synthetically generated peptide US-10-989-462-276
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/563,514
PRIOR FILING DATE: 2004-04-19
NUMBER OF SEQ ID NOS: 319
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97, Application US/10452593; Publication No. US20040258699A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IISYDGSKKYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VISYDGSKKYYADSVKG 66
                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: human
US-10-364-743-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-452-593-97
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GENERAL INVUMENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF52322
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PLING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-19
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2000-06-16
PRIOR PLING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1114

LENGTH: 251
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                                                                                                                                                                                                                                       Query Match

98.9%; Score 87; DB 10; Length 251;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels
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Publication No. US20050220795a1
Publication No. US20050220795a1
APPLICAT: Wittrup, K. Dane
APPLICANT: Yeung, Yik Andy
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01997-329001
CURRENT FILIAGO DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/520,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
98.9%; Score 87; DB 15; I
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1114, Application US/10293418; Publication No. US20030223996A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 VISYDGSKKYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                      1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                            TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-293-418-1114
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                                                                                                                                                                                               US-09-880-748-1114
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PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 135
                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: human
US-10-452-593-97
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Score 86; DB 16; Length 135; Pred. No. 1.9e-05; 1; Mismatches 0; Indels 1 IISYDGSKKYYADSVKG 17 :||||||||||||| 52 LISYDGSKKYYADSVKG 68 Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative

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RESULT 14

US-09-824

US-09-824

Sequence 24, Application US/09828708

APPLICANT: Ditzel, H.

APPLICANT: Button, D.

APPLICANT: Button, D.

APPLICANT: Button, D.

TITLE OF INVENTION: Autoimmune disease

TITLE OF INVENTION: autoimmune disease

FILE REFERENCE: 1361.005US1

CURRENT APPLICATION NUMBER: US/09/828,708

CURRENT PILLING DATE: 2011-09-24

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 17

TYPE: PRT

CREATH: 17

Length 17; Query Match 95.5%; Score 84; DB 9; L Best Local Similarity 88.2%; Pred. No. 4.7e-06; Matches 15; Conservative 2; Mismatches 0;

1 IISYDGSKKYYADSVKG 17

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Gaps ö

RESULT 15
US-10-630-009-24
; Sequence 24, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Button, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate isomerase and their partici;
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate isomerase and their partici;
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate;
; TITLE OF INVENTION: Autcantibodies to glucose-6-phosphate;
; FILE REFERENCE: 1341.065U52
; CURRENT APPLICATION NUMBER: US/10/630,009
; PRIOR PILING DATE: 2001-04-06
; NUMBER: OF SEQ ID NOS: 123
; SOFTWARE: PASTESQ for Windows Version 4.0
; SEQ ID NO 24
LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-24

Length 17; Query Match
Best Local Similarity 88.2%; Pred. No. 4.7e-06;
Matches 15; Conservative 2; Mismatches 0

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Search completed: October 14, 2005, 17:00:42 Job time: 121.859 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 23.6406 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-11 88 1 IISYDGSKKYYADSVKG 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283416 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES																														
SUM	er er	PL0120	844115	PL0116	<b>S29546</b>	PH1646	PH1644	PH1643	ᇁ	538490	463	846392	836270	831677	831116	F36005	531112	<b>\$19666</b>	G36005	E36005	831119	S38493	PL0098	m	831679	М	831701	PH1642	m	Ξ
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	Length	94	97	98	98	109	109	111	111	113	114	114	117	118	118	119	120	121	121	122	122	123	130	132	134	139	137	108	114	119
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	Score	82	82	82	82	82	82	82	82	85	82	82	82	82	82	82	82	82	82	82	85	85	82	82	82	82	77	75	75	75
	Result No.	н	7	e	4	ហ	9	7	œ	6	10	11	12	13	14	15	.16	17	18	19	20	21	22	23	24	25	56	27	28	59

heavy chain	heavy	heavy chain	heavy chain	heavy	heavy chain	heavy chain		heavy chain	heavy	Ig heavy chain v r					
117	797	028	831510	529543	6259	PH1662	M3HUAM	S31688	598	S70442	A60943	S36284	PH1661	PH1660	1592
8313	848797	A49028	831	\$2	83	표	M3	833	831	370	<b>A</b> 6(	836	H	PH	831
7	7	7	~	~	7	7	-	7	~	~	~	~	7	~	~
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.2 122 2	.2 128 2	7	~	.1 98 2	.1 117 2	.1 118 2	-	.1 134 2	.1 135 2	.1 140 2	.0 151 2	.8 115 2	.8 121 2	118 2	~
85.2 122 2	85.2 128 2	85.2 133 2	85.2 133 2	.1 98 2	84.1 117 2	84.1 118 2	84.1 122 1	84.1 134 2	84.1 135 2	84.1 140 2	83.0 151 2	81.8 115 2	81.8 121 2	80.7 118 2	78.4 76 2

### ALIGNMENTS

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RESULT 2
344115
Ig heavy chain V region - human
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C; Date: 13-Jan-1995 #sequence_results
R; Hawkins: R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable relatives number: S44115
A; Accession: S44115
A; Status: preliminary
A; Andlecule type: DNA
A; Residues: 1-97 - HAM
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

ö Query Match 93.2%; Score 82; DB 2; Length 97; Best Local Similarity 88.2%; Pred. No. 7.5e-06; Matches 15; Conservative 1; Mismatches 1; Indels

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Gaps

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"Ig heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1643
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone 6H12) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1646
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 2-4-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1644
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Mulb. 33301610; PMID:8315388
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A;Accession: PH209: mRNA
A;Mclecule type: mRNA
A;Residues: 1-109 cH11.x
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9UL93
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.4e-06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels
                                 Indels
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   Pred. No. 7.5e-06;
1; Mismatches 1;
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88.2%;
      88.24;
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Best Local Similarity 88.2.
Best Local Si Conservative
                                        15; Conservative
Best Local Similarity
Matches 15; Conserv
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A; Residues: 1-109 <HIL>
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                                                                                                                                                                                                                     igheavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PLO116; 82689;
R;Bird, J; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J; Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PLO116; MUID:88286083; PMID:2840480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Reaidues: 1-98 < TONA
A; Reaidues: 1-98 < TONA
A; Reaidues: 1-98 < TONA
A; Cross-references: BEBL: Z17394; NID: 932843; PIDN: CAA78997.1; PID: 932844
A; Note: designated COS-8
A; Note: designated COS-8
B; Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of NA; Reference number: S26885; MUD: 93021117; PMID: 1404388
A; Accession: S26888
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-98 -BIR>
A; Residues: 1-98 -BIR>
A; Residues: 1-98 -BIR>
A; Residues: 1-98 -BIR>
A; Experimental Bource: B cells from patient AW with acute lymphoblastic leukemia, ALL A; Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement R; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Reference number: $26885; MUID: 93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bete: 07-Jan-199 4# #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S;9546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Reference number: S29546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID:g32913
A,Note: designated DP-46
C,Superfamily: immunoglobulin V region; immunoglobulin homology
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88.2%; Pred. No. 7.5e-06;
tive 1; Mismatches 1;
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                                                     1 IISYDGSKKYYADSVKG 17
                    1 IISYDGSKKYYADSVKG 17
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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us-10-614-959-11.rpr

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Greater Homo sapiens (man)
C;Species: Homo sapiens (man)
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36276
A;Reference number: S36276
A;Reference number: S36276
A;Reference number: S36276
A;Reference number: MRIL
A;Reference number: MRIL
A;Residues: 1-17 cGRI>
A;Cross-references: EMBL: Z18839; NID:933118; PIDN:CAA79291.1; PID:9939898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (VH-28) - human
C;Species: Homo'sapiens (man)
C;Species: Homo'sapiens (man)
C;Species: Homo'sapiens (man)
C;Species: Homo'sapiens (man)
C;Species: Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46392
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J, Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by )
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Reference preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:231688; NID:g499306; PIDN:CAA83493.1; PID:g1335145
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
      Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: 846390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by JRAccession: 846390
A;Reference number: 846390
A;Accession: $46390
A;Accession: $46390
A;Accession: $46390
A;Accession: $46390
A;Accession: $46390
A;Cross-references: EMBL:231686; NID:9509782; PIDN:CAA83491.1; PID:91335143
C;Superfeamlly: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 88.2
Matches 15; Conservative
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Matches 15, Conservative
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S46392
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S36270
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PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1645
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc A;Accession: PH1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S38490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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A;Residues: 1-13 < MR>
A;Residues: 1-13 < MR>
Cross-references: EMEL:Z23030; NID:g414027; PIDN:CAA80565.1; PID:g414028
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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A;Molecule type: mRNA
A;Residues: 1-111 <HILD:
A;Cross-references: UNIPROT:O8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-111 <HIL>
A; Residues: 1-111 <HIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 7-90/Domain: immunoglobulin homology <IMM>
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88.2%; Pred. No. 8.7e-06;
iive 1; Mismatches 1; Indels
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1larity 88.2%; Pred. No. 8.6e-06;
Conservative 1; Mismatches 1; Indels
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Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1;
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nes 15; Conservative
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nes 15; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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Best Loca Matches

RESULT 10 S46390

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1; Indels

Score 82; DB 2; Length 119; Pred. No. 9.2e-06;

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A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene f
A;Reference number: A36005, MUD:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:QBWUK1; GB:M34026
C;Genetics: A6cenes: GDB:118731; OMIM:146910
A;Cross-references: GDB:118731; OMIM:146910
A;Cross-references: GDB:118731; OMIM:146910
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INM>
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88.2%; Pred. No. ...
1; Mismatches
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Best Local Similarity 88.2
Matches 15; Conservative
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R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
Ry Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A; Reference number: S31104; MUID:92111633; PMID:1730252
A, Accession: S31116
A, Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-118 cRAA
A; Residues: 1-118 cRAA
A; Rosidues: 1-118 cRAA
A; Cross-references: UNIPROT: QBWUK1; EMBL: X62966
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Saccession: 831677
R.Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R.Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A.Description: Mechanisms that generate human immunoglobulin diversity operate from the A.Reference number: 831585
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C;Species: 02-Dec_1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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A;Status: preliminary
A;Status: preliminary
A;Residues: 1-118 <CUI>
A;Crose:references: EMBL:Z14172; NID:g31009; PIDN:CAA78541.1; PID:g31010
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                       93.2%; Score 82; DB 2; Length 117;
88.2%; Pred. No. 9e-06;
iive 1; Mismatches 1; Indels
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88.2%; Pred. No. 9.1e-06;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 2; I
Pred. No. 9.1e-06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                               RESULT 13
S31677
Ig heavy chain V region - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 VISYDGSNKYYADSVKG 66
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                                                                                                                                                                    SO VISYDGSNKYYADSVKG 66
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.2'
Matches 15; Conservative
                         Query Match
Best Local Similarity 88.2°
Matches 15; Conservative
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Matches
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October 14, 2005, 15:51:44; Search time 113.156 Seconds (without alignments) 76.932 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                 Run on:
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US-10-614-959-11 88 1 IISYDGSKKYYADSVKG 17

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		sapien	sapien	sapien	sapien	sapien	Bapien	sapien	sapien	sapien	sapien	sapien	sapien	sapien	Bapien	sapien	sapien	sapien	ng lae	sapien	sapien	sapien	sapien	sapien	carassius a	sapien	xenopus lae	sapien	Bapien	sapien	sapien	sapien
		homo	homod	homod	homod	homod	homo	homod	homod	homod	рошо	homod	homod	homo	рошо	homod	homod	ношо	xenopus	homod	homod	рошо	рошо	homo	caras	homod	xenop	homo	homo		homo	рошо
Degration	1	Q9u193	Q65zc9	O8wuk1	09n190	P01768	O6n093	Q68cn4	Q9y509	Q7z351	Q8nc16	Q9u184	P01773	09u1b6	P01769	Q6pja4	06pi81	P01770	Oedda7	P01771	Q6n092	Q9u171	06pj95	Q9u172	P19181	P01772	O6inm5	Q60097	O6mzu6	69 <b>9</b> 60	P01762	P01767
2						z							z		z			z		z					5	z					7.	z
		Senre3	Q652C9	QBWUK1	D9UL90	HV3G HUMAN	26N0 <u>9</u> 3	D68CN4	29Y509	072351	DBNCL6	29UL84	HV3L HUMAN	OBULB6	HV3H_HUMAN	Q6PJA4	Q6PI81	HV3I_HUMAN	260007	HV3J HUMAN	Q6N092	29UL71	26PJ95	09UL72	HV05 CARAU	HV3K_HUMAN	OGINMS	760N9Q	56MZU6	296BB9	HV3A_HUMAN	HV3F_HUMAN
DB	; ; ,		N	N	~	-	~	~	'n	N	~	~	-	'n	_	~	'n	_	N	_	~	~	N	~	_	_	'n	_	0	~	۳ ٦	
Length		116	240	613	113	122	417	493	147	482	493	122	119	95	122	470	478	119	614	121	519	121	544	118	116	126	593	481	464	597	122	115
Query Match		33.2	93.2	93.2	84.1	84.1	80.7	79.5	78.4	76.1	76.1	75.0	73.9	72.7	72.7	72.7	72.7	71.6	71.6	70.5	70.5	69.3	69.3	٠	•	63.6	63.6	62.5	60.2	60.2	59.7	59.1
Score		20	82	82	74	74	71	70	69	67	67	99	65	64	64	64	64	63	63	62	62	61	61	09	26	26	26	22	23	23	52.5	25
Result No.		7	8	m	4	'n	ø	7	α .	σ ;	10	נו:	12	13	14	15	16	17	18	19	50	21		23	24	25	56	27	28	29	30	31

Q6in78 homo sapien Q6mzq6 homo sapien Q6gmz2 homo sapien P01763 homo sapien P01763 homo sapien Q920e7 mus musculu Q65218 mus musculu Q6gpx4 xenopus lae Q9gj71 salmo trutt Q9gy71 salmo trutt Q9gy73 salvo P18528 mus musculu P01764 homo sapien Q6n94 homo sapien Q6n94 homo sapien Q6n94 homo sapien	
Q6IN78 Q6MZQ6 QCGMXZ HV3B HUMAN Q920E7 Q65ZLB Q65ZLB Q6GY1 Q94V3 HV57 MOUSE HV3C HUMAN Q6NO94 YC81 METJA	
88888888888888888888888888888888888888	
466 476 4933 1119 1119 711 87 98 117 117 1048	
559 11 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	
4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
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ALIGNMENTS

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Single-chain Fv (Fragment). Name=acFv; Homo aspiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.

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Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98277139; PubMed-9614934; DOI-10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
PIR; PH1642; PH1642.

R PIR; PH1643; PH1643.

R PIR; PH1643; PH1643.

R PIR; PH1645; PH1645.

R PIR; PL0029; PH1645.

R PIR; PL0120; PL0120.

DR PIR; S1119; S1119.

DR PIR; S31119; S31119.

DR PIR; S70442; S70442.

DR PEAM; PF07654; C1-8et; 4.

SMART; SM0406; IGV; 1.

DR PROSITE; PS00290; IG MHC; UNKXNOWN 3.

PROSITE; PS00290; IG MHC; UNKXNOWN 3.

PROSITE; PS00290; IG MHC; SOWN; 60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                  Query Match
93.2%; Score 82; DB 2; Length 613;
Best Local Similarity 88.2%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON-TER 113 113
SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035024; AAD56260.1; --
PIR, S79486; S78486.
HSSP; PO1772; ZEB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SNART; SM00406; IGY; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                            1 IISYDGSKKYYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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HV3G_HUMAN
ID HV3G HUMAN
AC P01768;
DT 21-JUL-1986 (1
DT 21-JUL-1986 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young D.C.;
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                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGHM protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                           93.2%; Score 82; DB 2; Length 240; 88.2%; Pred. No. 2.3e-05;
                                       SEQUENCE FROM N.A.
STRAIN=11q/7;
MINDLINE=37362799263;
KONTERMANN R.E., Wing M.G., Winter G.;
Complement recruitment using bispecific diabodies.";
Nat. Biotecchnol. 15:629-631(1997).
Mat. Biotecchnol. 15:629-631(1997).
MinterPro; 1PR0013599; Ig.
InterPro; 1PR001359; Ig.
InterPro; 1PR001359; Ig.
InterPro; 1PR00409; IG. 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
NON TER 240 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: 8202040; AAH20240.1; -.
PIR; F36005; F36005.
                                                                                                                                                                                                                                                                                           240 240
240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 AA
                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IISYDGSKKYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 88.29
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                            SEQUENCE
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Query Match 80.7%; Score 71; DB 2; Length 417; Best Local Similarity 70.6%; Pred. No. 0.0029; Matches 12; Conservative 4; Mismatches 1; Indels

1 IISYDGSKKYYADSVKG 17 :|:|||| :|||||:| 22 VIAYDGSTQYYADSVRG 38

PROSITE; PSS0835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
NON_TER 1 1 1
SEQÜENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

STKRR

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2 Te:39:19 2005
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                                                                                                                              (1)

SEQUENCE.

MEDLINE=81013859; PubMed=6774332;

A Lehman D. W., Putnam F.W.;

Tocation of a possible JH segment.";

Tocation of a possible JH segment.";

Proc. Natl. Acad. Sci. U.S.A. 77:323-3243(1980).

LI Proc. Natl. Acad. Sci. U.S.A. 77:329-3243(1980).

Pattent with macroglobulinemia.

- I - MISCELLANEOUS: This mu chain was isolated from the plasma of a pattent with macroglobulinemia.

- I - SIMILARITY: Contains 1 immunoglobulin-like domain.

PR: A02051; M3HJOA.

PR: PIR: A02051; M3HJOA.

R GO: GO:000555; F:antigen binding; NAS.

GO: GO:000555; P:immune response; NAS.

GO: GO:000555; P:immune response; NAS.

MENDETC: IPRO07110; IG-1ike.

MENDETC: IPRO07110; IG-1ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.1%; Score 74; DB 1; Length 122; Best Local Similarity 70.6%; Pred. No. 0.00024; Matches 12; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig-like.
Pyrrolidone carboxylic acid.

        DOMAIN
        1
        112
        19-like.

        MOD_RES
        1
        1
        Pyrrolidone carboxylic ac:

        NON_TER
        122
        122
        SEQUENCE
        122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin V region;
            05-JUL-2004 (Rel. 44, Last annotation update) Ig heavy chain V-III region CAM. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP00047; 19; 1. SMART; SM00406; IGv; 1. PROSITE; PS50815; IG LIKE; 1. Direct protein sequencing; Im Pyrrolidone carboxylic acid.
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OGBCN4 PRELIMINARY; PRT; 493 AA.

25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotherical protein DKFZp686523209 (Fragment).
Name=DKRZp686523209;
Name=DKRZp686523209;
BURATYCIA MARMALIA: Entheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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417 AA

TISSUERCE FROM N.A.

TISSUERCETUM tumor;

TISSUERCETUM tumor;

TISSUERCETUM tumor;

The German consortium;

Bloccker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,

A Ganger A., Fobo G., Han M., Wiemann S.;

Submitted (Aud.22004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR749861; CA418705.1;

IN EMPL; CR749861; CA418705.1;

IN InterPro; IPR003159; IG_-1.

IN InterPro; IPR003159; IG_-1.

IN InterPro; IPR003159; IG_-1.

IN INTERPRO; IPR003106; IG_-1.

IN FF007654; C1-8et; 3.

Pfam; PF007654; C1-8et; 3.

Pfam; PF007654; C1-8et; 3.

R PROSITE; PS00409; IG_-1.

R PROSITE; PS00409; IG_-1.

R PROSITE; PS00409; IG_-MHC; UNKNOWN_2.

M PROSITE; PS00209; IG_-MHC; UNKNOWN_2.

THE CATALING AUG.

THE CATALING

TISSUE FROM N.A.

TISSUE-Human esophagus tumor;

TISSUE-Human esophagus tumor;

The German Human cDNA Consortium;

The German Human cDNA Consortium;

Mambut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Robo G., Han M., Wiemann S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640623; CAR45777.1; -..

REMBL; BX640623; CAR45777.1; -..

REMBL; BX6703599; IG.

InterPro; IPR003109; IG.

InterPro; IPR003106; Ig.—Hke.

RINGERPO; IPR003106; Ig.—Hke.

RINGERPO; IPR003106; Ig.—Hke.

RINGERPO; IPR003595; Ig.

RINGERPO; IPR003595; Ig.

RINGERPO; IPR003106; Ig.—Hke.

RINGERPO; IPR003106; Ig. G6N093;
G5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein DKF2p686104196 (Fragment).
Name-DKF2p686104196;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. PRELIMINARY; Q6N093 OF NO 93
OF

Gapa ö 79.5%; Score 70; DB 2; Length 493; 70.6%; Pred. No. 0.0052; Live 4; Mismatches 1; Indels Created) Last sequence update) Last annotation update) 147 AA PRT; :|||:| |::|||||| 92 VISYEGGKQHYADSVKG 108 Q9Y509 Q9Y509; 01-NOV-1999 (TrEMBLrel. 12, Cr 01-NOV-1999 (TrEMBLrel. 12, La 01-OCT-2003 (TrEMBLrel. 25, La VH3 protein (Fragment). 1 IISYDGSKKYYADSVKG 17 Query Match Best Local Similarity 70.67 Matches 12, Conservative Homo sapiens (Human) ઠે

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493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;

SEQUENCE

Eukaryota; Metazoa; Chordata, Cranlata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RESULT 8 Q9Y509

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Local Similarity 81.2%; Pred. No. 0.0053;
Les 13; Conservative 1; Mismatches 2; Indels
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ90170.
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HSSP, P01772, 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PR0STIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%; Score 67; DB 2; 70.6%; Pred. No. 0.016; tive 3; Mismatches
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Homo sapiens (Human).
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Best Local Similarity
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                        NCBI_TaxID=9606;
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SEQUENCE
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Matches
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                                                                                  MEDLINE=96071149; PubMed=7475288; Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C., Lichtenstein A.K., Berenson J.R.; A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers."; Leukemia 9:1948-1953(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PESSUE-Human rectum tumor;
A Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Boecher M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

R FODO G., Han M., Wiemann S.;
R HSSP; PO1857; 1HZH.
R InterPro; IPR003106; 19 MHC.
R InterPro; IPR003597; 19 G.1.
R InterPro; IPR003506; 19 MHC.
R R InterPro; IPR003506; 19 MHC.
R PROSITE; PS50835; 1G LIKE; 4.
R PROSITE; PS50835; 1G LIKE; 4.
R PROSITE; PS50835; 1G LIKE; 4.
R PROSITE; PS00290; 1G LIKE; 4.
Hypothetical protein.
C SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                        BMBL; 980866; AAD14339.1; ...
HSSP; P01842; 1AQK.
GQ; GQ:0005887; Cintegral to plasma membrane; NAS.
GQ; GQ:0016066; P:cellular defense response (sensu Vertebrata); NAS.
InterPro; IPR003110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SMO0406; IGV: 1.
NON_TER 1475; IG LIKE; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.4%; Score 69; DB 2; Length 147; 76.5%; Pred. No. 0.002; artive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686N02209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 76.1%; Score 67; DB 2; Local Similarity 70.6%; Pred. No. 0.016; es 12; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 76.5
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                               SEQUENCE FROM N.A.
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        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQÜENCE
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QBNCL6
ID QBNCL6
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Q72351

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RESULT 9

Matches

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Gaps

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493 AA

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PRELIMINARY;

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72.7%; Score 64; DB 2; Length 95; 75.0%; Pred. No. 0.0087; tive 1; Mismatches 3; Indels

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Query Match
Best Local Similarity 75.0%
Matches 12; Conservative
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HV3H_HUMAN
ID HV3H_HUMAN
AC P01769;
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W MEDLINE=79151016; PubMed=107164;

W MEDLINE=79151016; PubMed=107164;

A Putnam F.W., Liu Y.-S.Y., Low T.L.K.;

Putnam F.W., Liu Y.-S.Y., Low T.L.K.;

IT IgAl protease, digestion, Fab and Fc fragments, and the complete amino and sequence of the alpha 1 heavy chain.";

I IgAl protease, digestion, Fab and Fc fragments, and the complete amino and sequence of the alpha 1 heavy chain.";

I Islo. Chem. 254:2865-2874 (1979).

IL J. Biol. Chem. 255; Alflura.

IL J. Biol. Chem. 255; Alflura.

IL J. Biol. Chem. 255; Alflura.

IL J. SIMILARITY: Contains 1 immunoglobulin-like domain.

R ISSP: PO1772; ZEB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005925; P:immune response; NAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR00710; Ig-like.
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                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
IG heavy chain V-III region BUR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig.v.
Prime, PF00047; ig. 1.
SWART; SWART; SW00406; IGv. 1.
PROSITE; PS50815; IGv. 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
MOD RES 1 19-1ike.
MOD RES 1 19-1ike.
DISTURID 22 96
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28 28 N-linked (GlcNac. .).
119 119
119 Aa; 12981 MW; 12A709A75344D024 CRC64;
                                                                                                                                                                                            119 AA
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             2 ISYDGSKKYYADSVKG 17
                                       51 ISNDGSNKFYADSVKG 66
                                                                                                                                                                                         STANDARD;
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                                                                                                                               RESULT 12
HV3L HUMAN
AC P01773;
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 05-JUL-2004
DE IG heavy chains
OC EURARYCTA;
RN MEDLINE=7915;
RN GO; GO:00059;
DR GO; GO:00059;
DR GO; GO:00059;
DR GO; GO:00059;
DR HORFPRO; IPI
DR PRAM; PROOUF
DR P
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Matches
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Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM immunoglobulins.";
Blochemierry 13:2482-2488-1974).
-!- MISCELLANEQUS: This chain was isolated from a Waldenstrom's

MEDLINE=74175307; PubMed=4208843;

NCBI_TaxID=9606;

SEQUENCE

macroglobulin.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PTR, A02052, M3HUGA.
HSSP, PO1772; ZPB4.
GO; GO:0003823; P: entracellular; NAS.
GO; GO:0003852; P: entracellular; NAS.
GO; GO:0005955; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
105-JUL-2004 (Homan V-III region GA.

122 AA.

PRT;

STANDARD;

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                                                                                               Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                  122 122
122 AA; 13166 MW; 74E5B6959E84100A CRC64;
PERMIT PRODUCT 19. 1.
SMART; SM0040; 1Gv; 1.
DROSITE; PSS035; 1GLIKE; 1.
Driect protein sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 112 19.
MOD_RES 1 1 1 Pyrrolidone carboxylic NON_TER 122 12.
SEQÜENCE 122 AA; 13166 MW; 74ESB6959E84100A CRC6
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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50 VISYBGBBZYYAASVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                               OGPJA4;
05-UUL-2004 (TrEMBLrel. 27,
05-UUL-2004 (TrEMBLrel. 27,
05-UUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                         Local Similarity 64.7 tes 11, Conservative
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ID O6
AC O6
DT O5
DT O5
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

099ULB6 11D QQ 000 DT 001 001 DD 001 002 DT 001 003 DT 001 003 DT 001 004 DT 001 005 DT

GJULB6; GJULB6; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Imunoglobulin heavy chain (Fragment).

95 AA.

PRELIMINARY;

Q9ULB6

SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Tange Y., Kayano H.;
Submitred (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO352568; BAA87067.1; -.
PIR; PH0872; PH0872.

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TISSUE FROM N.A.

TISSUE Primary B-Cells,

TISSUE Primary B-Cells,

TISSUE Primary B-Cells,

TISSUE Primary B-Cells,

TISSUE BELTK PLONGE 12477912; DOI=10.1073/pnas.242603899;

X Alausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Alausher R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Alachul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toehlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Alakesley R.W., Touchman U.W., Garcia A.N., Gay L.J., Hulyk S.W.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Diakesley R.W., Touchman J.W., Gamen E.D., Dickson M.C.,

A Diakesley R.W., Touchman J.W., Gamen E.D., Dickson M.C.,

A Diakesley R.W., Touchman J.W., Gamen E.D., Dickson M.C.,

A Diakesley R.W., Touchman J.W., Gamen E.D., Myers R.W., Butterfield Y.S.,

A Diakesley R.W., Mala M.J., Sanilus D.E., Schnerch A., Schein J.E.,

A Dones S.J., Marra M.A.;

Tomes S.J., Marra M.A.;

Tomes S.J., Marra M.A.;

The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
               Homo Gapiene (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.7%; Score 64; DB 2; Length 470; 75.0%; Pred. No. 0.05; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 470 AA; 51715 MW; 7B49556AllFD7D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Primary B-Cells;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                         Mammalia; Eutheri
NCBI_TaxID=9606;
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2 ISYDGSKKYYADSVKG 17 ઠે

Local Similarity 75.0 nes 12; Conservative

Best Loca Matches

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Gaps

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Search completed: October 14, 2005, 16:19:51 Job time : 115.156 seca

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October 14, 2005, 15:51:19; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-12 50

1 ASIAAARVLDY 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2105692 Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2031s:*

7: geneseqp2031s:*

8: geneseqp2031s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES 쮼

Description	Aav79070 Anti-fact				. (1	ហ	_	N			9 209	Amin							-	-	•	•		•		Aaw00780 Thermitas
a.		AAY79077	ADJ48827	AA013448	ADS26132	ADS25655	ADS25373	ADS22602	ABB48560	AAG18510	AAG18509	AAY37904	ADS28058	AAG20306	AAG51887	AAP80850	AAP80274	AAR54838	AAW00768	AAW00769	AAW00774	AAW00798	AAW00770	A & WOOD 775	07/00#44	AAWUU/BU
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Query Match	•	92.0	74.0	72.0	72.0	72.0	72.0	N	0	8	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	0.89		•
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ALIGNMENTS

AAY79070 standard; peptide; 11 AA.

(first entry) 12-JUN-2000

Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence

Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CBRG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 03-MAR-1999; 28-AUG-1998;

(GETH) GENENTECH INC

ä Kirchhofer Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the heavy chain variable domain of a human anti-factor IX/Ixa Gla domain antibody. Factor IXA/Ixa da vitamin K dependent plasma serine procease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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This sequence represents a complementarity determining region 3 (CDR3) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial cells and platelets. Compositions comprising the antibodies are used for the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is
the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary artery bypass graft (thrombosis), percutaneous transluminal coronary angloplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity determining region 3; CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.
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                                                                                                                                                                                                                                                      Length 11;
                                                                                                                                                                                                                                100.0%; Score S0; DB 3; Length 11
100.0%; Pred. No. 0.003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hass PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY79077 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eaton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 2; 84pp; English.
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                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                   1 ASIAAARVLDY 11
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                                                                                                                                                                                                                                                                                                                                                          Devaux B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-256595/22.
                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                      Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams CW,
                                                                                                                                                                                                                                                            Query Match
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The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic plant seed.
indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (AROS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                   oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
62;
                                                                                                                                                      Score 46; DB 3;
Pred. No. 0.019;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Oil-associated gene related protein #327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 831; 22pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Savage T,
                                                                                                                                                                                                                                                                                                                      ADJ48827 standard; protein; 408 AA.
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26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
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80.0%;
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                                                                                                                                                      92.0%;
90.9%;
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RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                            1 ASIAAGRVLDY
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Best Local Similarity
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Best Local Similarity
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                                                                                                                             Sequence 11 AA;
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26-JUN-2002;
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(SAVA/)
(LEDE/)
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

Bacterial polypeptide #15165.

(first entry)

02-DEC-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to Oytokine. Call prollferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
     Gaps
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     IndelB
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     Mismatches
                                                                                                                                                                AA013448 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                             Human polypeptide SEQ'ID NO 27340.
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                       (first entry)
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275 ASLAAARALD 284
                                      1 ASIAAARVLD 10
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
                                                                                                                                                                                                                                         06-NOV-2001
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Matches
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 15165; 122pp; English.

Goldman BS;

Chen X,

Cao Y, Hinkle GJ, Slater SC,

WPI; 2004-061375/06.

(CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P.

US2003233675-A1.

.8-DEC-2003.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soppear. The method of producing a transformed plant cauch as maize or soppear. The method of producing a transformed plant cauch as maize or soppear. Occuping the transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme camping conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydare, introgen or providing improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress condition, improved plants production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form form or interprofucion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.0
Best Local Similarity 63.6
Matches 7; Conservative
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ADS26132 standard; protein; 652

ADS26132 ID

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Gaps

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72.0%; Score 36; DB 4; Length 58; 70.0%; Pred. No. 12; 1; Indels tive 2; Mismatches 1; Indels

Local Similarity 70.0

Best Loca Matches

Query Match

2 SIAAARVLDY 11 |:| ||||:| SVAQARVLEY 21

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Sequence 652 AA;

a

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255 AATAAARAIDY 265
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ADS25655 standard; protein; 652 AA Bacterial polypeptide #14688. (first entry) US2003233675-A1. 02-DEC-2004 Bacteria. ADS25655

cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. Recombinant DNA construct; transformed plant; improved plant property;

18-DEC-2003

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P

HINKLE G J. SLATER S C. CHEN X (CHEN/) (CAOY/) (SLAT/) (HINK/

Chen X, Slater SC, Hinkle GJ, Cao Y,

GOLDMAN B S.

Goldman BS

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 14688; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promote a provide defect a polynoucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or producing plants with improved plant properties, e.g. improved cold, heat or progens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the grope of the invention. Note: The sequence data for this patent did not form at from USPTO at segdata.uspto.gov/sequence.html.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant bank construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant cut as maize or soppears. The method of producing a transformed plant construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the colympost or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or a drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rappose increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

WPI; 2004-061375/06

Claim 1; SEQ ID NO 14406; 122pp; English

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                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                 Gaрв
                 ö
Length 652;
Score 36; DB 8; Length 652
Pred. No. 1.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                           Chen X,
                                                                                                   ADS25373 standard; protein; 655 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                     20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                                                      21-FEB-2002; 2002US-0360039P.
                                                                                                                                                       Bacterial polypeptide #14406
 72.0%;
                                                                                                                                      02-DEC-2004 (first entry)
 Query Match 72.0
Best Local Similarity 63.6
Matches 7; Conservative
                                              |: |||| :||
255 AATAAARAIDY 265
                                    1 ASIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                             HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                           GOLDMAN B S.
                                                                                                                                                                                                                                                                  JS2003233675-A1.
                                                                                                                                                                                                                                                                                   18-DEC-2003.
                                                                                                                     ADS25373;
                                                                                                                                                                                                                                                 Bacteria.
                                                                                                                                                                                                                                                                                                                                                                  (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                            Cao Y,
                                                                                                                                                                                                                                                                                                                                        CAOY/)
                                                                                                                                                                                                                                                                                                                                                          (SLAT/)
                                                                                                                                                                                                                                                                                                                                                  HINK/)
                                                                                  RESULT 7
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least one stress providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html. 88888888888

Sequence 655 AA;

72.0%; Score 36; DB 8; Length 655; 63.6%; Pred. No. 1.6e+02; ive 2; Mismatches 2; Indels Local Similarity 63.6 1 ASIAAARVLDY 11 Query Match Best Loc Matches

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Gaps

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|: |||| :|| 255 AATAAARAIDY 265 a

ADS22602 standard; protein; 656 AA. Bacterial polypeptide #11635. 02-DEC-2004 (first entry) ADS22602;

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

Bacteria.

US2003233675-A1.

18-DEC-2003

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P

CAO Y. HINKLE G J. SLATER S C. CHEN X. CAOY/) (HINK/)

GOLDMAN B S. (SLAT/) (CHEN/) (GOLD/)

Chen X, Goldman BS; Hinkle GJ, Slater SC, Cao Y,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 11635; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant with the having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with

improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.

Sequence 656 AA

Gapa ö Score 36; DB 8; Length 656; Pred. No. 1.7e+02; 2; Mismatches 2; Indels 72.0%; 63.6%; Query Match Best Local Similarity 63.64;

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|: |||| :|| 255 AATAAARAIDY 265 1 ASIAAARVLDY 11 셤 ò

ABB48560 standard; protein; 708 AA. ABB48560 ID ABB4

(first entry) 05-FEB-2002

Listeria monocytogenes protein #1264.

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.

Listeria monocytogenes.

WO200177335-A2

18-OCT-2001.

11-APR-2001; 2001WO-FR001118.

11-APR-2000; 2000FR-00004629.

(INSP) INST PASTEUR

Cossart P; Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart F Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.

Claim 6; SEQ ID NO 1265; 192pp; French.

of L The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins

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expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially blosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
                      8$8888888888888
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Gaps ö 70.0%; Score 35; DB 5; Length 708; 75.0%; Pred. No. 2.9e+02; cive 2; Mismatches 0; Indels ||||::|| 697 AAARIIDY 704 4 AAARVLDY 11 Best Loc Matches ઠે 셤

Sequence 708 AA;

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Zea mays protein fragment SEQ ID NO: 19948. AAG18510 standard; protein; 157 AA 17-OCT-2000 (first entry) AAG18510; RESULT 10

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.

Zea mays subsp. mays

EP1033405-A2

25-FEB-2000; 2000EP-00301439 06-SEP-2000

25-FEB-1999; 05-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 16-APR-1999; 19-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 06-MAY-1999; 06-MAY-1999; 06-MAY-1999;

99US-0121825P.
99US-012180P.
99US-0125188P.
99US-0125788P.
99US-0125788P.
99US-0125787P.
99US-0126785P.
99US-012874P.
99US-013874P.
99US-013144P.
99US-013144P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P. 14-MAY-1999; 14-MAY-1999; 14-MAY-1999;

9905-0134941P 9905-0135629P 9905-0135629P 9905-0135621P 9905-0136621P 9905-0136621P 9905-0136621P 9905-0137524P 9905-0137524P 9905-0137524P 9905-0137524P 9905-0137524P 9905-0137624P 9905-0137624P 9905-0139453P 9905-0139453P 9905-0139453P 9905-0139453P 9905-0139454P 9905-0139454P 9905-0139454P 9905-0139453P 9905-0139458P 9905-0139458P 9905-014085P 9905-014085P 9905-014085P 9905-014085P 9905-014333P 9905-014433P 9905-014432P 9905-014433P 13. July 1999) 14. July 1999) 15. July 1999) 16. July 1999) 16. July 1999) 19. July 1999) 19. July 1999) 19. July 1999) 18 - 70N - 1999 22 - 70N - 1999 23 - 70N - 1999 24 - 70N - 1999 25 - 70N - 1999 26 - 70N - 1999 27 - 70N - 1999 28 - 70N - 1999 29 - 70N - 1999 29 - 70N - 1999 01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 09-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 26-JUL-1999; 27-JUL-1999; 27-JUL-1999; 18-MAY-1999; 19-MAY-1999; 20-MAY-1999; 21-MAY-1999; 25-MAY-1999; 25-MAY-1999; 26-MAY-1999; 20-JUN-1999; 40-JUN-1999; 10-JUN-1999; 10-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 118-JUN-1999; 118-JUN-1999; 19-JUL-1999 30-JUN-1999

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Gaps

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Query Match 68.0%; Score 34; DB 3; Length 157; Best Local Similarity 100.0%; Pred. No. 90; Matches 7; Conservative 0; Mismatches 0; Indels

99US-0161359P. 99US-0161360P. 99US-0161361P. 99US-0161920P. 99US-0161993P. 99US-0161993P.

26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 28-0CT-1999; 28-0CT-1999; 29-0CT-1999;

990S-0145919P. 990S-0145919P. 990S-0146386P. 990S-0146388P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0147304P. 990S-0148684P. 990S-0148684P. 990S-0148684P. 990S-0149304P. 990S-0149304P. 990S-0149304P. 990S-0150864P. 990S-0150864P. 990S-0150864P. 990S-0150864P. 990S-0150864P. 990S-0151304P. 990S-0151034P. 990S-0157313P. 990S-0157865P. 27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 04-AUG-1999; 04-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 21-AUG-1999;

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.

Zea mays subsp. mays

EP1033405-A2

06-SEP-2000

2000EP-00301439

25-FEB-2000;

Zea mays protein fragment SEQ ID NO: 19947

entry)

(first

17-OCT-2000

AAG18509;

AAG18509 standard; protein; 159 AA.

RESULT 11 AAG18509

117 AARVLDY 123

8

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5 AARVLDY 11

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07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
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15-8EP-1999 20-8EP-1999 20-8EP-1999 20-8EP-1999 20-8EP-1999 20-8EP-1999 20-8EP-1999 20-6CT-1999 13-6CT-1999 13-6CT-1999 14-6CT-1999 14-6CT-1999 14-6CT-1999 14-6CT-1999 15-6CT-1999 16-6CT-1999 17-6CT-1999 18-6CT-1999 19-6CT-1999 19-6C

25-FEB-1999; 05-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 16-APR-1999; 16-APR-1999; 13-APR-1999; 13-APR-1999; 13-APR-1999; 13-APR-1999; 14-APR-1999; 14-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 1999; 25-MAY-1999; 25-MAY-1999; 25-MAY-1999; 25-MAY-1999; 25-MAY-1999; 25-MAY-1999; 25-MAY-1999;

99US-0121825P.
99US-0123180P.
99US-012548P.
99US-0126264P.
99US-012624P.
99US-0128234P.
99US-0128234P.
99US-0128234P.
99US-012845P.
99US-0130449P.
99US-0130448P.
99US-0131449P.
99US-0131449P.
99US-0131449P.
99US-0131449P.
99US-013149P.
99US-013149P.
99US-013248PP.
99US-013248PP.
99US-013488P.

us-10-614-959-12.rag

RR 28-MAY-1999; RR 01-JUN-1999; RR 03-JUN-1999; RR 04-JUN-1999; RR 10-JUN-1999; RR 16-JUN-1999; RR 16-JUN-1999; RR 18-JUN-1999; RR 23-JUN-1999; RR 24-JUN-1999; RR 24-JUN-1999; RR 25-JUN-1999; RR 25-JUN-1999; RR 26-JUN-1999; RR 27-JUN-1999; RR 27-JUN-1999; RR 27-JUN-1999; RR 23-JUN-1999; RR 24-JUN-1999; RR 25-JUN-1999; RR 25-JUN-1999; RR 25-JUN-1999; RR 25-JUN-1999; RR 25-	US-0136782P US-0137222P US-0137222P US-0137724P US-0138094P US-0138840P US-0139452P US-0139452P US-0139454P US-0139454P US-0139454P US-0139455P	99US-0139457P. 99US-013458P. 99US-0139458P. 99US-0139461P. 99US-0139461P. 99US-0139461P. 99US-0139463P. 99US-0139463P. 99US-0139463P. 99US-013963P. 99US-0140351P. 99US-0140351P. 99US-0140351P. 99US-0141287P. 99US-0141287P. 99US-0141287P. 99US-0141287P. 99US-0141287P. 99US-0141289P. 99US-014139P. 99US-0141331P. 99US-01440055P. 99US-01440055P. 99US-01440055P. 99US-01440055P. 99US-01440055P. 99US-0144331P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P.	905 - 01448141 905 - 01450861 905 - 01450851 905 - 01450871 905 - 0145181 905 - 01452181 905 - 014522181 905 - 014522181 905 - 014522181 905 - 014522181 905 - 014532181 905 - 0145381 905 - 01463881 905 - 01463881 905 - 01463881 905 - 01463881
	28 - MAY - 1999 01 - JUN - 1999 03 - JUN - 1999 04 - JUN - 1999 08 - JUN - 1999 10 - JUN - 1999 14 - JUN - 1999 16 - JUN - 1999 17 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999	18-70N-1999 18-70N-1999 18-70N-1999 18-70N-1999 18-70N-1999 18-70N-1999 18-70N-1999 23-70N-1999 23-70N-1999 23-70N-1999 23-70N-1999 23-70N-1999 23-70N-1999 23-70N-1999 24-70N-1999 29-70N-1999 29-70N-1999 29-70N-1999 13-70N-1999	21 - JUL - 1998 21 - JUL - 1998 22 - JUL - 1999 22 - JUL - 1999 22 - JUL - 1999 23 - JUL - 1999 23 - JUL - 1999 24 - JUL - 1999 27 - JUL - 1999 28 - JUL - 1999 29 - JUL - 1999 20 - AUG - 1999 02 - AUG - 1999 03 - AUG - 1999 04 - AUG - 1999

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990S-0147132P.
990S-0147132P.
990S-0147303P.
990S-0147303P.
990S-0147313P.
990S-0147931P.
990S-0147931P.
990S-014932B.
990S-014932B.
990S-0149722P.
990S-0149722P.
990S-0149722P.
990S-014972P.
990S-014972P.
990S-014972P.
990S-015103P.
990S-015923P.
990S-015923P.
990S-015923P.
990S-015923P.
990S-015923P.
990S-015923P.
990S-016932P.
04-NUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
10-AUG-1999;
11-AUG-1999;
11-AUG-1999;
12-AUG-1999;
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13-AUG-1999;
14-AUG-1999;
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16-SEP-1999;
16-SEP-1999;
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18-CCT-1999;
18-CCT-1999;
18-CCT-1999;
18-CCT-1999;
18-CCT-1999;
18-CCT-1999;
19-CCT-1999;
11-CCT-1999;
12-CCT-1999;
12-CCT-1999;
13-CCT-1999;
14-CCT-1999;
15-CCT-1999;
16-CCT-1999;
17-CCT-1999;
18-CCT-1999;
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us-10-614-959-12.rag

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

Bacterial polypeptide #17091.

02-DEC-2004 (first entry)

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ADS28058;

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AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogramulomatosis. The polypeptides of the invention may be of use in treating these diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                  Gaps
                                                                                                                  ö
                                    68.0%; Score 34; DB 3; Length 159; 100.0%; Pred. No. 91; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 1426; 1755pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY37904 standard; protein; 180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97FR-00015041.
97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1999 (first entry)
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis
                                                                                                                                                                                                                      |||||||
119 AARVLDY 125
                                                                                                                                                                             5 AARVLDY 11
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04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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XX

AC

AAY37904

XXX

AAY37904

XXX

AAY37904

XXX

AAY37904

XXX

AAY37904

AAY3704

AAY3704

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 17091; 122pp; English.

Goldman BS;

Chen X,

Hinkle GJ, Slater SC,

Cao Y,

WPI; 2004-061375/06.

(CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P.

US2003233675-A1.

18-DEC-2003.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant with the ecombinant DNA construct and growing the transformed plant with the correction or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with inproved plant properties, e.g. improved cold, heat or a facught tolerance, collarance to herbicides, extreme osmotic conditions, pathogens or peats, increased resistance to plant disease, better growth rate by modification of the content, improved yield by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of forbotosynthesis or by production, improved light, production or improved galactomannan condition, improved light, by modification or improved galactomannan condition, improved light production or improved galactomannan compant of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic correct of the printed specification but was obtained in electronic correct of the printed specification but was obtained in electronic correct of the printed specification but was obtained in electronic correct of the printed specification but was obtained in electronic correct of the printed specification but was obtained in electronic correct of the printed specification but was obtained in electronic corrections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Gaps

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Length 180; 1; Indels

68.0%; Score 34; DB 2; 77.8%; Pred. No. 1e+02; tive 1; Mismatches

Local Similarity 77.8

Query Match Best Loc Matches ||||| :|| 140 IAAARSMDY 148

3 IAAARVLDY 11

RESULT 13 ADS28058 ID ADS28058 standard; protein; 231 AA.

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                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 22440
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                                                                                                                  entry)
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100 ATIAAARKLD 109
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Similarity 100.0%; Pr
7; Conservative 0;
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Query Match
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11 AARVLDY

₹ RESULT 15 AAGS1887 ID AAG51887 standard, protein, 237

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 65899

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana

EP1033405-A2

06-SEP-2000

25-FEB-2000; 2000EP-00301439

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Search completed: October 14, 2005, 16:12:40 Job time : 85.5625 secs

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513545 seqs, 74649064 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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US-09-383-667-19
; Sequence 19, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Baton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Hass, Philip E.
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2

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Sequence 6, Application US/07849420;
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Retent No. 5989856
GENERL INFORMATION:
APPLICANT: van dev Ven, Willem Jan Marie
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Robroek, Antonius Johannes Maria
TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor);
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFEILER Plaza
Endoproteolytic Activity, A Process for
Endoproteolytically Processing (Precursor)
Proteins And For The (Micro)Biological
Production Of Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2; Length 278;
Pred. No. 25;
0; Mismatches 2; Indels
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COMPUTER: IDM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,203
FILING DATE: 29-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REGISTRATION NUMBER: 40,846
REGISTRATION NUMBER: 294-41 DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELECOMMUNICATIO
                                                                                                                                                                                            ADDRESSEE: HOFFMANN & BARON, LLP STREET: 350 Jericho Turnpike CITY: Jericho STAEE: New York COUNTRY: U.S.A. ZIP: 11753 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%;
80.0%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0
Matches 8; Conservative
      TITLE OF INVENTION: Endc
TITLE OF INVENTION: Prot
TITLE OF INVENTION: Prot
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-865-203-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ASILAVRVLD 105
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-849-420-6
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Pred. No. 30;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 4; Length 11;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Patent No. 5935815
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09342648

| Sequence 2, Application US/09342648
| Patent NO. 6248584
| GENERAL INFORMATION:
| APPLICANT: Cahoon, Rebecca E. APPLICANT: Cahoon, Rebecca E. APPLICANT: APPLICANT: APPLICANT: Rafalski, Antoni
| TITLE OF INVENTION Transcription Coactivators FILE REFRENCE BB-1169-B
| CURRENT FILING DATE: 1999-06-29
| CURRENT FILING DATE: 1999-06-29
| EARLIER APPLICATION NUMBER: 60/092,659
| EARLIER PILING DATE: July 13, 1998
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: Microsoft Office 97
| LENGTH: 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                  CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 19
LENGTH: 11
                    CURRENT APPLICATION NUMBER: US/09/383,667
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-383-667-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
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NAME/KEY: UNSURE
LOCATION: (179)
FEATURE:
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LOCATION: (241)
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US-08-865-203-6
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US-08-955-424-6
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APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: van buijnhoven, Johannes Lambertus Petrus;
APPLICANT: Robroek, Antonius Johannes Maria; and
APPLICANT: Roning, Piet Nico Maria
ITILE OF INVENTION: Pharmaceutical Composition Having An
ITILE OF INVENTION: Endoproteolytically Processing (Precursor)
ITILE OF INVENTION: Proteins And For The (Micro)Biological
ITILE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: HOFFMANN & BARON, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NAMBE: US/07/849,420
FLING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MOTAN, Thomas F.
REGISTRATION NUMBER: 2805/41413
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEGUENCE A 22523
TELERAS: 422523 COOP UI
INFORMATION FOR SEG ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
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ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/253,854
FILING DATE: Unassigned
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-253-854-6; Sequence 6, Application US/09253854; Patent No. 6132717; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: HOFFMANN & BARON, 350 Jericho Turnpike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-07-849-420-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 ASILAVRVLD 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
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APPLICANT: Van de Ven, Willem Jan Marie
APPLICANT: Van de Ven, Willem Jan Maria Wilhelmina
APPLICANT: Van de Ouweland, Anna Maria Wilhelmina
APPLICANT: Van de Ouweland, Anna Maria Wilhelmina
APPLICANT: Van duijhnoven, Johannes Lambertus Petrus
APPLICANT: Koning, Piet Nico Maria
APPLICANT: Roebroek, Antonius Johannes Maria
TITLE OF INVENTION: PERCURSOR) PROCESS FOR ENDOPROTEOLYTICALLY PROCESSING
TITLE OF INVENTION: PRODUCTION OF PROTEINS
FILE REFERENCE: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
CURRENT APPLICATION NUMBER: US/08/955,424
CURRENT APPLICATION NUMBER: 07/849,420
EARLIER APPLICATION NUMBER: 07/849,420
EARLIER PILING DATE: 1992-06-12
EARLIER PILING DATE: 1992-06-12
EARLIER PILING DATE: 1990-10-21
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
SEG IBROEK NUMBER: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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US-09-135-658-4

i Sequence 4, Application US/09135658

j Sequence 4, Application US/09135658

j Patent No. 5972683

j GENERAL INFORMATION:
    APPLICANT: TSAL, Ying-Chieh
    TITLE OF INVENTION: MUTANT TYPE SUBTILISIN YAB AND ITS APPLICATION
    FILE REPERENCE: 6653-011-999
    CURRENT APPLICATION NUMBER: US/09/135,658
    CURRENT PILING DATE: 1998-08-18
    EARLIER APPLICATION NUMBER: 86112766
    EARLIER PILING DATE: 1997-09-04
    NUMBER OF SEQ ID NOS: 8
    NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                         Score 34; DB 3; Length 278;
Pred. No. 25;
0; Mismatches 2; Indels
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80.0%; Pred. No. 25;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-955-424-6
Sequence 6, Application US/08955424
Patent No. 6274365
GENERAL INFORMATION:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPPOLOGY: linear
; MOLECULE TYPE: protein
US-09-253-884-6
                                                                                                                                                                                                                                                68.0%;
80.0%;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Matches 8; Conservative
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96 ASILAVRVLD 105
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LENGTH: 279
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, ORGANISM: Bacillus
US-09-196-281-9
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5472855-6
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                                                                 Score 34; DB 2; Length 279;
Pred. No. 25;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%; Score 34; DB 4; Length 279;
80.0%; Pred. No. 25;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6. Application US/09515150A
Settle No. 6558938
GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Rim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5348.204.US
CURRENT PILING DATE: 2000-02-29
CURRENT PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                    US-09-512-251A-6

Sequence 6, Application US/09512251A

Sequence 6, Application US/09512251A

Sequence 6, Application US/09512251A

GENERAL No. 655355

GENERAL NO. 655355

FAPLICANT: Hansen, Peter

APPLICANT: Makeleen, Frank

APPLICANT: Andersen, Kim

TITLE OF INVENTION: Processe Variants and Compositions

FILE REPRENCE: 5349.204-US

CURRENT APPLICATION NUMBER: US/09/512,251A

CURRENT FILING DATE: 2000-02-24

NUMBER: PATENTING DATE: 2000-02-24

SOFTWARE: PATENTIN VERSION 3.1
                                                                       Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-135-658-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.0
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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96 ASILAVRVLD 105
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                                                                                                                                               1 ASIAAARVLD 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-512-251A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 4; Length 279;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
Sequence 9. Application US/09196281A

Sequence 9. September 10. 6605488

GENERAL INFORMATION:
APPLICANT: Hansen, Peter K.
APPLICANT: Hansen, Peter K.
TITLE OF INVENTION: Protease Variants And Compositions
FILE REFERENCE: 5435.200-US
CURRENT FILING DATE: 1999-11-19
CURRENT FILING DATE: 1997-11-21
MUMBER OF SEQ ID NOS: 18
SOFTWARE FELLS FELLS 1987-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE FELLS FELLS FELLS 1997-11-21
LENGH': 279
LENGH': 279
LENGH': 279
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19472855
1972855-
1972855-
1972856-
1972871: CARTER, PAUL J.;WELLS, JAMES A.
17171E OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,964
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 90,902
FILING DATE: 14-JAM-1993
APPLICATION NUMBER: 823,039
FILING DATE: 14-JAM-1992
APPLICATION NUMBER: 334,081
FILING DATE: 06-APR-1987
APPLICATION NUMBER: 334,081
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 127,134
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 866,627
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 886,534
FILING DATE: 20-ARY-1984
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.v.
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1 ASIAAARVLD 10 ||| | ||||

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RESULT 15
US-09-710-279-622
i Sequence 622, Application US/09710279
; Sequence 622, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT; KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTON: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SEQ ID NO 622
; SEQ ID NO 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: synthetic
CTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.0%; Score 33; DB 4; Length 194; 60.0%; Pred. No. 26; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                   Score 33; DB 4; Length 85;
Pred. No. 9.8;
1; Mismatches 2; Indels
CTHER INFORMATION: Gap in alignment;
PEATURE:
NAME/KEX: MISC FEATURE
NOAME/CATION: (30)...(33)
OTHER INFORMATION: Gap in alignment
US-09-698-286A-10
                                                                                                                                                                                             Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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106 NVASASVLDY 115
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71 SIAAGKPLDY 80
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                                                         RESULT 13
5472855-6
i Patent No. 5472855
i Patent No. 5472855
i TILLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,964
FILING DATE: 22-SEP-1994
FRING APPLICATION DATA:
APPLICATION NUMBER: 90,902
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 823,039
FILING DATE: 06-APR-1987
APPLICATION NUMBER: 35,652
FILING DATE: 06-APR-1989
APPLICATION NUMBER: 127,134
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 846,627
FILING DATE: 01-ARR-1986
APPLICATION NUMBER: 866,534
FILING DATE: 20-ARR-1986
APPLICATION NUMBER: 614,612
FILING DATE: 20-MAY-1984
APPLICATION NUMBER: 614,612
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
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Search completed: October 14, 2005, 16:22:01 Job time : 22.6562 secs

US-09-698-286A-10

Sequence 10, Application US/09698286A

Patent No. 6677442

GENERAL INFORMATION:

APPLICANT: University of Kentucky Research Foundation

TITLE OF INVENTION: Human REV1 Gene and Protein As Diagnostic, Preventive, and Therap

TITLE REFERENCE: 050229-0247

CURRENT APPLICATION NUMBER: 05/162,140

PRIOR APPLICATION NUMBER: 60/162,140

PRIOR PILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 85

TYPE: PRT

VEGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
OCTRION: (17)...(22)
OTHER INFORMATION: Gap in alignment
FEATURE:

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Gapв

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SOUS US:85:01 C

96 ASILAVRVLD 105

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                 OM protein - protein search, using sw model
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October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec US-10-614-959-12 50 Title: Perfect score: Sequence: Run on:

1 ASIAAARVLDY 11

1859788 seqs, 416717961 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/DSOT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/NSOB_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/USIOB_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OI.	US-10-425-115-369042	US-10-389-566-831	US-10-425-114-45544	US-10-425-115-208229	US-10-425-115-208239	179-10-427-962-100369	0C/07T-C06-/CE-0T-C0	US-10-369-493-14688	US-10-369-493-15165	US-10-369-493-14406		US-10-369-493-11635	US-10-437-963-189048
DB	16	15	15	16	16	14	1		15				16
Query Match Length DB	183	408	573	573	694	1203		652	652	655		909	1064
Query Match	80.0	74.0	74.0	74.0	74.0	74.0		72.0	72.0	72.0		72.0	72.0
Score	40	37	37	37	37	3.7		9 7	36	36	20	9 1	36
Result No.	1	7	٣	4	S	9	r	- 1	20	σ	,	7;	11

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6	US-10-437-963-1752	US-10-767-701-38892	US-10-369-493-1709	US-10-336-324-6	-403-1	US-10-425-115-3534	US-10-767-701-45651	US-10-369-493-7093	US-10-369-493	US-10-425-114	US-10-437	US-10-437-963	US-10-238-075	US-10-724-972	US-10-032-585	US-10-425-114	US-10-156-761	US-10-282-122A-62	US-10-282-122A-6392	US-10-282-122A-62	US-10-282-122A-6483	US-11-058-046	US-10-627-476	US-09-738-626-6	US-10-36	US-10-437-963	US-10-417-700	US-10-282-122/	US-10-369-493	US-10-425	US-10-282-122A-63	US-10-152-886-53	US-11-053-576-5
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35	35	34	34	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	93	33	33	e i	33	33	33	33	33	33	33
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	e :	34	35	36	37	38	68	40	41	42	43	44	45

ALIGNMENTS

APPLICANT: La Rosa: Thomas J.
APPLICANT: La Rosa: Thomas J.
APPLICANT: Avair. David K.
APPLICANT: APPLICANT: Avair.
APPLICANT: Avair.
APPLICANT: Avair.
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53122)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 36942
LENGTH: 183 TYPE: PRT
COCALISM: Zea mays
COCALISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(183)
COTHER INFORMATION: unsure at all Xaa locations
FEATURE:
COTHER INFORMATION: Clone ID: MRT4577_99740C.1.pep
US-10-425-115-369042 ; Sequence 369042, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION: US-10-425-115-369042

Gaps ö Query Match 80.0%; Score 40; DB 16; Length 183; Best Local Similarity 90.0%; Pred. No. 7.9; Matches 9; Conservative 0; Mismatches 1; Indels 2 SIAAARVLDY 11 . 8

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91 SIAADRVLDY 100

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TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-425-115-208239
US-10-425-115-208229
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Sequence 45544, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Edu, Yihua
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Go, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 455544

LENGTH: 573
                                       Sequence 831, Application US/10389566
; Sequence 831, Application US/1038956
; Publication No. US20040025202A1
; GENERAL INFORMATION:
    APPLICANT: Monsanto Technology, LLC
    APPLICANT: Laurie, Cathy C
    TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TILE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TILE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
    CURRENT APPLICATION NUMBER: US 60/385,301
    PRIOR FILING DATE: 2002-06-25
    PRIOR FILING DATE: 2002-06-26
    NUMBER OF SEQ ID NOS: 2459
    SOCTWARE: PatentIn version 3.2
    SEQ ID NO 831
    LENGTH: 408
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// ICCATION: (103)...(104)

// OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-389-566-831
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74.0%; Score 37; DB 15; Length 408;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: 700800359_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASIAAARVLDY 11
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58 ANIADTRVLDY 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-114-45544
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APPLICANT: Language of the state of the stat
Sequence 208229, Application US/10425115

Sequence 208229, Application US/204272A1

Sequence 208229, Application No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Con Yihua

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-64-28

SEQ ID NO 208229

LENGTH: 573
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Pred. No. 1.38+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 16; Length 573;
Pred. No. 1e+02;
1; Mismatches 2; Indels
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US-10-425-115-208239
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US-10-425-115-208229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 72.7
Matches 8; Conservative
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Matches 8; Conservative
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Sequence 14406, Application US/10369493
; Sequence 14406, Application US/10369493
; Sequence 14406, Application No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Goody Yongwel
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR PRILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14406
; LEMATH. 6 FE
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: UNMER: US/10/369,493
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11635
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                                                                                                                                                                                                                                                                                                                                   Length 652;
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Pred. No. 1.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 36; DB 15; Length 65
63.6%; Pred. No. 1.9e+02;
tive 2; Mismatches 2; Indels
                  FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11165
LENGTH: 652
                                                                                                                                                                                                                      TYPE: PRT GRANISM: Agrobacterium tumefaciens US-10-369-493-15165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14406
                                                                                                                                                                                                                                                                                                                              72.0%;
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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255 AATAAARAIDY 265
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255 AATAAARAIDY 265
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US-10-369-493-14406
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Sequence 14688, Application US/10369493

Sequence 14688, Application US/10369493

Sequence 14688, Application US/10369493

Sequence 14688, Application US/10369493

SEQ IN VENTION

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianteng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT PAPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PLING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14688

LENGHIA 652
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120758
LENGTH: 1203
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US-10-169-493-15165

Sequence 15165, Application US/10369493

Sequence 15165, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative ;
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Best Local Similarity 63.6
Matches 7; Conservative
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255 AATAAARAIDY 265
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Gaps

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Score 35; DB 16; Length 45;
Pred. No. 18;
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
US-10-437-963-201347
                                                                                                                                                  0; Mismatches
                                                                                                   70.0%;
                                                                                                   Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                2 SIAAARVLD 10
                                                                                                                                                                                                                                            16 SIATARVLD 24
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NAME/KEY: unsure
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US-10-767-701-38892
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; Sequence 20147, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Wat wat
; APPLICANT: Wat wat
; APPLICANT: Wat wat
; APPLICANT: Li, Fing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201347
                                                                                                                                                                                                                                                                                                                                                                Sequence 189048, Application US/10437963
Sequence 189048, Application US/10437963
Publication No. USZ0040123343A1
Sequence 189088, Application US/20040123343A1
SENDERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 189048
LENGTH: 1064
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72.0%; Score 36; DB 16; Length 1064;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels (
                                                                                                                              Query Match 72.0%; Score 36; DB 15; Length 656; Best Local Similarity 63.6%; Pred. No. 1.9e+02; Matches 7; Conservative 2; Mismatches 2; Indels
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US-10-437-963-189048
                                         ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11635
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255 AATAAARAIDY 265
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ORGANISM: Oryza Bativa
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ORGANISM: Oryza sativa
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US-10-437-963-189048
                   LENGTH: 656
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Sequence 175236, Application US/10437963

Sequence 175236, Application US/10437963

Publication No. US20040123343A1

Sublication No. US20040123343A1

Sublication No. US20040123343A1

APPLICANT: Lace Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Applicant: Acid Wolecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221) B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 175236

LENGTH: 107
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Sequence 3892, Application US/10767701

Sequence 3892, Application No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Cao, Yougwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 38892

LENGTH: 198
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70.0%; Score 35; DB 16; Length 107;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236
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OTHER INFORMATION: unsure at all Xaa locations
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Page 5
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us-10-614-959-12.rapb
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RESULT 15
US-10-369-493-17091

is Sequence 17091, Application US/10369493

is Publication No. US20030233675A1

is GENERAL INPORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, USAPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

SEQ ID NO 17091

LENGTH: 231

LENGTH: 231
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                                                                                                                                        0; Gaps
                                                            Query Match 68.0%; Score 34; DB 16; Length 198; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17091
                                                                                                                                                                            5 AARVLDY 11
|||||||
114 AARVLDY 120
VUS-10-767-701-38892
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0; Gaps

Query Match 68.0%; Score 34; DB 15; Length 231; Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 8; Conservative 1; Mismatches 1; Indels

Search completed: October 14, 2005, 17:00:43 Job time: 79.2031 secs

1 ASIAAARVLD 10 |:||||| || 100 ATIAAARKLD 109

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-12 50 1 ASIAAARVLDY 11 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3-methylcrotonyl-C	3-methylcrotonyl-C	hypothetical prote	probable membrane	teichoic acid bios	carboxymethylenebu	thermitase (EC 3.4	methyltransferase	hypothetical prote	probable insulinas		DNA polymerase III	probable DNA polym	conserved hypothet	hypothetical prote	_			cobyrinic acid a.c	glycine dehydrogen	glutamyl-tRNA synt	membrane protein E	hypothetical prote	multidrug resistan	methionyl aminopep	_	hypothetical prote		N-carbamov1-beta-a
SUMMARIES	ID	AF2984	A98299	S43071	S56849	AE1210	D87715	SUMYTV	140371	T38883	B71468	AF1059	AF2831	B97609	F89878	G69213	T45400	C70858	C84904	A75619	H70463	G82104	845053	T27970	T06165	E85437	G69502	D64640	C87712	AG2869
	DB.	~	7	~	~	~	~	~	~	N	~	~	N	~	~	~	7	~	N	7	~	~	~	~	~	~	~	N	~	~
	Length	663	709	143	692	969	231	279	579	649	926	162	202	202	220	264	358	367	397	441	482	509	614	1027	1232	305	342	363	365	409
*	Query Match	72.0	72.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	8	99	0.99	99	99	0.99	99	99	0.99	0.99	99	66.0	0.99	99	99	64.0	64.0	64.0	64.0	64.0
	Score	36				32	34	34	34	34							33	33	33	33	33	33	33	33	33	32	32	32	32	32
	Result No.	1	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

n-carbamoyl-beta-a hypothetical prote hypothetical prote	probable ABC trans protein TINIS.9 (1 probable xanthine	hypothetical prote hypothetical prote hypothetical prote		glutathione transf electron transfer	conserved hypothet
A97646 T20819 T16256	B70558 G96524 G95940	T49642 T16347 AG2388	C75376 875615 B83036	AF3541 A81001 F82018	AC3018
000	100	0,00	0 0 0	0 0 0	10
415 435 448	576 655 777	817 119 131	144	230 249 249	254
64.0 64.0 64.0	64.0 64.0 64.0	62.0 62.0	62.0 62.0	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	62.0
322	352	32 31 31	31 31 31	31 31 31	31
30 31 32		36 33 38	39 4 4 0 1 1	4 4 4 2 6 4	4.5

ALIGNMENTS

"Ethylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (st C; Species: Agrobacterium tumefaciens 11-Jan-2002 #text_change 09-Jul-2004 [C; Accession: AF294] [A; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 [A; Athuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.

A/Itle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Ritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Retatus: Pretlaminary
A/Molecule type: DNA
A/Residues: 1-663 <KUR>
A/ROSSE-references: UNIPROT:08UA95; GB:AE008689; PIDN:AAL44292.1; PID:g17741880; GSPDB:GP
C/Genetics:

A;Gene: mccA A;Map position: linear chromosome C;Superfamily: propiony1-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy]

ö Gape ö Query Match 72.0%; Score 36; DB 2; Length 663; Best Local Similarity 63.6%; Pred. No. 27; Matches 7; Conservative 2; Mismatches 2; Indels

|: |||| :|| 258 AATAAARAIDY 268 1 ASIAAARVLDY 11 ò

RESULT 2

Ascient Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: A98299
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Aritle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUD:21608551; PMID:11743194
A;Accession: A98299
A;Accession: A98299
A;Accession: A88299
A;Kesidues: 1-709 <KUR>
A;Residues: 1-709 <KUR>
A;Cross-references: UNIPROT:Q8UA95; GB:AE007870; PIDN:AAK89915.1; PID:g15159866; GSPDB:GA
C;Genetics:
A;Genetics:

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70.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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245 SLAAAIILDY 254
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A;Accession: S47117
A;Molecule type: DNA
A;Residues: 135-692 <VAW>
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A Molecule type: DNA
A, Residues: 1-696 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AE1210
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A;Cross-treferences: EMBL:234288; NID:g498992; PIDN:CAA84049.1; PID:g498993
A;Cross-references: EMBL:234288; NID:g498992; PIDN:CAA84049.1; PID:g498993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
submitted to the EMBL Data Library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard
A;Reference number: S47117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-692 < ROS>
A; Residues: 1-692 < ROS>
A; Cross-references: UNIPROT: P40358; EMBL: Z49348; NID: 91008228; PID: 91008229; MIPS: YJL073
A; Cross-references: UNIPROT: P2; Portetelle, D.; Hilger, F.
R; Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
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A;Residues: 135-692 <POH>
A;Cross-references: EMBL:249348; MIPS:YJL073w
A;Cross-references: EMBL:249348; MIPS:YJL073w
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisia
A;Reference number: $50798; MUID:95282514; PMID:7762302
A;Accession: $50798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Mosdumes: 1-143 <THO>
A;Kesidumes: 1-143 <THO>
A;Kesidumes: 1-143 <THO>
A;Cross-references: UNIPROT:Q69582; EMBL:X73675; NID:g469952; FIDN:CAA52028.1; FID:g4699
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S43071
R;Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; Rc
Nocogene 9, 1167-1175, 1994
A;Title: A transforming fragment within the direct repeat region of human herpesvirus ty
A;Reference number: S43067; MUID:94181269; PMID:8134119
A;Accession: S43071
          A,Map position: linear chromosome
C,Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipo
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N.Alternate names: hypothetical protein HRC558; hypothetical protein J1083
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S56849; S56847; S50788; S47117; S57736
R;Rose, M.; Koetter, P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: human herpesvirus 6
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.0%; Score 35; DB 2; Length 143; 88.9%; Pred. No. 8.7; ative 1; Mismatches 0; Indels
                                                                                                 Query Match 72.0%; Score 36; DB 2; Length 709; Best Local Similarity 63.6%; Pred. No. 29; Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein 5 - human herpesvirus 6
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Matches 8; Conservative
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|ASLAAARVL 15
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87715
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolone
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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Cispecies: District and Cispecies
Cispecies: District and Cispecies
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Cispecies: Manageria Miles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 692,
A;Cross-references: EMBL:234288; NID:g498992; PID:g498993
R;Sor, F.J.
submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                           A,Reference number: S57731
A,Accession: S57756
A,Accession: S57756
A,Residues: 1-692 <SOR>
A,Cross-references: EMBL:X88851; NID:g895892; PID:g895898
C,Genetics: A,Gene: SGD:JEM1
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C;Ksywords: transmembrane protein
F;S85-655/Domain: dnaJ amino-terminal homology <DNJ>
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Pred. No. 45;
2; Mismatches
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hypothetical protein SPAC4H3.03c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T3883
B;Murphy, L; Harris, D; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: 221807
A;Accession: T38883
A;Accession: T38883
A;Accession: T38883
A;Accession: T38883
A;Accession: T38883
A;Accession: T3888
A;Residues: 1-649 < MUR>
A;Residues: 1-649 < MUR>
A;Residues: 1-649 < MUR>
A;Residues: 1-649 < MUR>
A;Coseinental source: strain 972h-; cosmid c4H3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Divideble insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW; C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Species: Charcesion: 13.468
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 198
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach A; Reference number: A71570; MUD:99000809; PMID:9784136
A; Status: preliminary
A; Molecule type: DNA.
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A;Cross-references: UNIPROT:O84812; GB:AE001353; GB:AE001273; NID:93329271; PIDN:AAC6840; A;Experimental source: serotype D, strain UM-3/Cx C;Genetics:
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R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MuID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SPDB:SPAC4H3.03c
A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2; Length 649;
Pred. No. 68;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ptr
C;Superfamily: insulin-degrading enzyme (IDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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631 AAIAAAHILD 640
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916 IAAARSMDY 924
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A;Molecule type: DNA
A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9A213; GB:AE005673; NID:g13425534; PIDN:AAK25720.1; GSPDB:G
C;Genetics:
A;Gene: CC3758
C;Superfamily: carboxymethylenebutenolidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Thermoactinomyces vulgaris
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A00973
R;MeLoun, B.; Baudys, M.; Kostka, V.; Hausdorf, G.; Frommel, C.; Hohne, W.E.
FEBS Lett. 183, 195-200, 1985
A;Title: Complete primary structure of thermitase from Thermoactinomyces vulgaris and it
A;Reference number: A00973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: profininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-579 <RES>
A;Cross-references: UNIPROT:P43423; EMBL:X79509; NID:g619638; PIDN:CAA56041.1; PID:g6196
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R;Rina, M.; Markaki, M.; Bouriotis, V.
Gene 150, 71-73, 1994
A;Title: Sequence of the cloned bseCIM gene: M.BaeCI reveals high homology to M.BanIII.
A;Reference number: 140371; MUID:95047552; PMID:7959066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 1-279 AEL>
A; Residues: 1-279 AEL>
A; Cross-references: UNIPROT: P04072
C; Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp. C; Superfamily: subtilisin; subtilisin homology
C; Keywords: hydrolase; serine proteinase
F; 29-239/Domain: subtilisin homology <SBT>
F; 29-239/Active site: Asp, His, Ser #status predicted
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                            Gaps
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C;Superfamily: site-specific methyltransferase (adenine-specific) PaeR7I
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                                                                                                                                                                                                                               Length 231;
                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methyltransferase - Bacillus stearothermophilus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermitase (BC 3.4.21.66) - Thermoactinomyces vulgaris
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                                                                                                                                                                                                                        Score 34; DB
Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          100 ATIAAARKLD 109
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ASILAVRVLD 105
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AEVIAKRILDY 36
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Best Local Similarity
Matches 6; Conserv
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Search completed: October 14, 2005, 16:23:38 Job time : 17.2969 secs
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54.5%;
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Local Similarity 60.0%;
les 6; Conservative
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94 ASIAAVKLINY 104
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131 NVASASVLDY 140
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                                           156 ASİAAARAL 164
1 ASIAAARVL
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A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97609
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Jaccesslon AF2831
C;Jaccesslon AF2831
C; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
F; Rapp, P; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable DNA polymerase III, epsilon chain [imported] - Agrobacterium tumefaciens (strai
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: Q8UDP4; GB: AE007869; PIDN: AAK87827.1; PID: 915157207; GSPDB: q
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: UNIPROT:QBUDP4; GB:AE008688; PIDN:AAL43068.1; PID:g17740536; GSPDB:
A.Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA polymerase III, epsilon subunit [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AF2831
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                             A;Molecule type: DNA
A;Residues: 1-162 <PAR>
A;Crosetres: 1-162 <PAR>
A;Crosetrics:
A;Gene: STY4801
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66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 202;
                                                                                                                                                                Score 33; DB 2; Length 162;
Pred. No. 26;
1; Mismatches 1; Indels
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88.9%; Pred. No. 32;
vative 0; Mismatches
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A;Map positTon: circular chromosome
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                                                                                                                                                                     66.0%;
75.0%;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                   6; Conservative
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112 AVARILDY 119
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                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-202 <KUR>
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A;Molecule type: DNA
A;Residues: 1-202 <KUR>
       Status: preliminary
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hypothetical protein MTH852 - Methanobacterium thermoautotrophicum (strain Delta H)
CiSpecies: Methanobacterium thermoautotrophicum
CiSpecies: Methanobacterium thermoautotrophicum
CiSpecies: Methanobacterium thermoautotrophicum
CiSpecies: Methanobacterium thermoautotrophicum
CiDate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
CiAccession: G69213
CiDate: Methanobacterium thermoautotrophicum Delta H: Missinth, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Paterence number: A69000; MUID:98037514; PMID:9371463
A; Accession: G69213
A; Accession: G69213
A; Accession: G69213
A; Accession: Methanobacterium thermoautotrophicum Delta H: functi
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-264 «MTH>
                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: F89978
A;Status: preliminary
A;Molecule type: DN.
A;Rosidus: 1-220 «KUR»
A;Residus: 1-220 «KUR»
A;Crosa-references: UNIPROT:Q99V10; GB:BA000018; PID:g13700889; PIDN:BAB42185.1; GSPDB:GP
A;Experimental source: strain N315
C;Genetics: SA0939
C;Superfamily: conserved hypothetical protein MG323
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A;Experimental source: strain Delta H
conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                        C; Accession: F89878
R; Kurcda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (R; Kurcda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2011
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
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Pred. No. 43;
4; Mismatches 1; Indels
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Pred. No. 35;
3; Mismatches
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October 14, 2005, 15:51:44; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                    Title:
Perfect :score:
Sequence:
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US-10-614-959-12 50 1 ASIAAARVLDY 11 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	O6h820 orvza sativ	2 shewan		orvza		_					Q69x93 oryza sativ	2 human	_		P40358 saccharomyc			-								O9fv51 arabidopsis			P43423 bacillus st	bacillus	oryza sat
ΩI	Д6Н820	Q8EFS2	Q8S2E4	Q8GU81	Q62CX8	Q63M18	QBUA95	Q7CSK5	Q8H034	Q7MA36	Q69X93	Q69582	Q6AQ91	Q9RJR7	YJH3 YEAST	Q8Y8 <u>3</u> 3	Q6MK31	Q7R034	Q6NA42	Q9A213	THET_THEVU	Q6AH23	OSZSTI	Q8ZXL8	Q9LS05	Q9FV51	Q8P7L4	Q8PIY6	MTC1_BACST	Q9RQK2	Q7F1D1
ength DB	421 2		1203 2				•		723 2	778 2		143 2	184 2	329 2	692 1	696 2	1228 2	6977 2	153 2	231 2	279 1	322 2	342 2	342 2			568 2	568 2	579 1	579 2	589 2
Query Match Length	74.0	74.0	74.0	74.0	72.0		72.0	72.0	72.0	72.0	72.0	70.0			70.0	70.0	0.07	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	œ.	θ.	æ.	68.0
Score	37	37	37	37	36	36	36	36	36	36	36	32	32	35	32	35	32	32	34	34	34	34	34	34	34	34	34	34		34	34
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		Vaalio bacceroldes Q7ezja oryza sativ O84812 chlamydia t Q8zxpl pyrobaculum	Q8zyb9 pyrobaculum Q8zl29 salmonella Q8zk37 salmonella Q83ss1 salmonella
Q7QH89 YAY3 SCHPO Q6ZG <u>0</u> 0	Q6FY30 Q67R60 Q8ZWI9	Q7EZJ3 Q7EZJ3 Q8ZXP1	Q82189 Q82129 Q82K37 Q83SS1
242	0 0 0 0	9000	0000
596 649 827	866 874 912 920	945 945 1206	162 162 162 162
68.0 68.0	00000	9 9 9 9	0000
334	0 0 0 0 0 4 4 4	. 4 4 4 4 4	* ጠ ጠ ጠ
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ALIGNMENTS

RESULT 1

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									daos																		; 0	
	PRELIMINARY; PRT; 421 AA.	,		2004 (TrEMBLrel. 27, Last sequence update)	2004 (TrEMBLrel. 27, Last annotation update)	GCN5-related N-acetyltransferase-like.	Name=OJ1297 C09.4;	ativa (japonica cultivar-group).	ta; Viridiplantae; Streptophyta; Embryophyta: Tracheor	ophyta; Magnoliophyta; Liliopsida; Poales: Poaceae:	Ehrhartoideae; Oryzeae; Oryza.	NCBI_TaxID=39947;		SEQUENCE FROM N.A.	Sasaki T., Matsumoto T., Yamamoto K.;	ed (AUG-2001) to the EMBL/GenBank/DDBJ databases.	EMBL; AP004087; BAD25129.1;	0008080; F:N-acetyltransferase activity; IEA.	GO; GO:0016740; F:transferase activity; IEA.	o; IPR000182; GCN5acetyl trans.	InterPro; IPR000504; RNA rec mot.	P00583; Acetyltransf 1; 1.	PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.	rase.	E 421 AA; 44979 MW; 7A9968BFFC673920 CRC64;	Query Match 74.0%; Score 37; DB 2; Length 421; Best Local Similarity 80.0%; Pred. No. 69;	1; Mismatches 1; Indels	
20	Q6H820	1	02-00F-5004	05-JUL-2004	05-JUL-2004	GCN5-re	Name=O1	Oryza B	Eukaryo	Spermat	Ehrhart	NCBI Ta	_ [<u>T</u>]	SEQUENC	Sasaki	Submitt	EMBL; A	 8 69	99;	InterPr	InterPro	Pfam; Pi	PROSITE	Transferase.	SEQUENCE	Query Match Best Local	Matches	
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RESULT 2
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ID QBEFS2
AC QBEFS
DT 01-M
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DT 01-M
DE ACET
GN STREW
(1)
RRP STRU
RC STRA
RRESULT
RX MEDL

QBEFS2 PRELIMINARY, PRT, 694 AA.

QBEFS2,

QBEFS

(1) SEQUENCE FROM N.A. STRAIN=MR-1; MEDLINE-22297686; PubMed=12368813; DOI=10.1038/nbt749;

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MDR-like ABC transporter.
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les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=mdr17
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Matches
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Sortt J., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., Mhite O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M., Lee C., Melson R.J., Khouri H.M., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Shewanella oneidensis."; Shewanella oneidensis."; Shewanella oneidensis."; I. Nat. Blotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12447438; DOI=10.1038/nature01184;

PubMed=12447438; DOI=10.1038/nature01184;

Sasaki T. Matsumoto T., Yanamoto K., Sakata K., Baba T., Katayose Y.,

Sasaki T., Matsumoto T., Yanamoto K., Sakata K., Baba T., Katayose Y.,

Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,

Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,

Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,

Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iroh Y., Iwabuchi A., Kamiya K.,

Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,

Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,

Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,

Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%; Score 37; DB 2; I
54.5%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 000874; F:Biotin binding; IEA.
GO; GO: 0008152; F:Biotin binding; IEA.
GO; GO: 0008152; P:Biotin binding; IEA.
InterPro; IPR001892; Biotin_BS.
InterPro; IPR001892; Biotin_BS.
InterPro; IPR0005481; GPase L.N.
InterPro; IPR0005481; GPase L.N.
InterPro; IPR0011053; Biotin_lipoyl.
InterPro; IPR011054; CPhyla Guntif.
Pfam; PF02785; Biotin_arab C; 1.
Pfam; PF02785; Biotin_arab C; 1.
Pfam; PF00289; GPSase L. Chain; 1.
Pfam; PF00289; GPSase L. Chain; 1.
PROSITE; PS00189; BIOTIN; 1.
PROSITE; PS00189; BIOTIN; 1.
PROSITE; PS00189; BIOTIN; 1.
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SEQUENCE 694 AA; 75656 N
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Best Local Similarity 54.5
Matches 6; Conservative
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Name=P0022F10.15;
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                                                                                                                                                                                                                                                                                                                   HSSP; P24182; 1DV1.
TIGR; SO1894; -
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Gaps ö 74.0%; Score 37; DB 2; Length 1234; 70.0%; Pred. No. 2e+02; Live 2; Mismatches 1; Indels 1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64; Pfam; PF00664; ABC membrane; 2.
Pfam; PF00065; ABC tran; 2.
Probom; PD000006; ABC transporter; 2.
PROSITE; PS50929; ABC TMIF; 2.
PROSITE; PS00211; ABC TRANSPORTER 1; 2.
PROSITE; PS50893; ABC TRANSPORTER 2; 3.
ATP-binding.
SEQUENCE 1234 AA; 134571 MW; CSF9E9D7; InterPro; IPR003439; ABC_transporter. Local Similarity 70.0 1 ASIAAARVLD 10 Query Match **datches**

||:|| |:|| 330 ASVAATRILD 339

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Distribute 2034;

Nierman W.C. DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
Bavidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Structural flexibility in the Burkholderia mallei genome.";
Froc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

EMBL; CP000011; AAU46877.1;
-. SEQUENCE 402 AA; 41596 MW; 6FCA16BE0F4B1BEA CRC64; Burkholderia mallei ATCC 23344. Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia. NCBI_TaxID=243160; 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Major facilitator superfamily protein.
ORFNames=BMAA0712; 402 AA PRT; PRELIMINARY; 23344; SEQUENCE FROM N.A. RESULT 5
062CX8
10 062C
AC 062C
AC 062C
DT 25-0
DT 25-0
DE Majo
CS Burk
OC Bur

ö Length 402; 72.0%; Score 36; DB 2; Length 402 70.0%; Pred. No. 1.1e+02; ative 3; Mismatches 0; Indels Query Match 72.0 Best Local Similarity 70.0 Matches 7; Conservative

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1 ASIAAARVLD 10

|::||||:|| 106 ATVAAARLLD 115

RESULT 6

063M18 PRELIMINARY, PRT, 402 AA. 25-0CT-2004 (TrEMBLrel. 28, Last sequence update) 25-0CT-2004 (TrEMBLrel. 28, Last sequence update) 25-0CT-2004 (TrEMBLrel. 28, Last annotation update)

SEQUENCE FROM N.A.

STRAIN=K96243;

Putative transporter protein.
ORFNames=BPSS0842;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia. 063M18 11D QQQ DT 222 DT 222 DT 222 DG GN DT 222 DG CN DT 2222 DG CN DT 2222
ö PubMed=15377794;

Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Arthin T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
A Chilingworth T., Croin A., Crosset B., Davis P., DeShazer D.,
Reitwill T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Reith K.E., Maddison M., Moule S., Price C., Quall M.A.,
Rabbinowitsch E., Rucherford K., Sanders M., Simmonds M.,
Songsivilai S., Stewnes K., Tumapa S., Vesaratchaves M.,
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Rucholderia pseudomallei.",
Proc. Natl. Acad. Sci. U.S. 101:14240-14245(2004).
EMBL, BX571966; CAH38304.1; -. Сарв ö Query Match 72.0%; Score 36; DB 2; Length 402; Best Local Similarity 70.0%; Pred. No. 1.1e+02; Matches 7; Conservative 3; Mismatches 0; Indels 1 ASIAAARVLD 10 ઠે

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|::||||:|| 106 ATVAAARLLD 115

RESULT 7 **Q8UA95**

Agrobacterium tumefaciena (atrain CS8 / ATCC 33970). ascteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobiaceae; Rhizobiaceae; Mizobiaceae; Mizobiaceae; Misobiaceae; Misobi Q8UA95 PRELIMINARY; PRT; 663 AM.
Q8UA95;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
3-mechyl-crotonyl-cod carboxylase alpha subunit.
Name-mccA; OrderedLoousNames=Atul3479;
Name-mccA; OrderedLoousNames=Atul3479; SEQUENCE FROM N.A.

STRAIN-Dupont;

WELINE-21608550; PubMed=11743193; DOI=10.1126/science.1066804;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Rutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Annag S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Cordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.;

"The genome of the natural genetic engineer Agrobacterium tumefaciens

Science 294:2317-2323(2001). EMBL, AE009278; AAL44292.1; -. PIR; A98239; A98299. PIR; AF2984; AF2984.

HSSP, P24182, IBNC.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000374; F:bictin binding; IEA.

GO; GO:00016874; F:ligase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

Pfam; PF00785; Bictin_carb C; 1.

Pfam; PF00785; Bictin_lipoyl; 1.

Pfam; PF00789; CSsase L. chain; 1.

PROSITE; PS00188; BIOTIN; 1.

PROSITE; PS00186; CPSASE I; UNKNOWN 1.

PROSITE; PS00186; CPSASE I; UNKNOWN 1.

Bictin; Complete proceome.

SEQUENCE 663 AA; 71187 MW; 2366201C5F

71187 MW; 2366201C5F36D292 CRC64;

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SEQUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,

Wing R.A., Yu Y., Soderlund C., Kim H.-R., Spiegel L., Preston R.,

Collura K., McCombie D.W.R., de la Bastide M., Spiegel L., Preston R.,

Kirchoff K., Kuit K., Nascimento L., Zutavern T., Balija V., Bell M.,

Baker J., Santos L., Miller B., Katzenberger F., Muller S., King L.,

Yang C., O'Shaugnessy A., Palmer L., Dedhia N.;

Submitted (JAN 2003) to the EMBL/GenBank/DDBJ databases.

EMBL; ACI19796, AAO17354.1;
Hypothetical protein OJ1172F09.9.

Name=OJ1172F09.9;

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;

Ehrhartoldese; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 723 AA; 78613 MW; 3FD842215E6ED1FD CRC64;
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InterPro; IPR008938; ARM.
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Q7MA36
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=2160851; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Esp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Good C., Sear C., Strub G., Glenome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CS8.";
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                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2; Length 709;
Pred. No. 1.8e+02;
2; Mismatches 2; Indels
            Score 36; DB 2; Length 663;
Pred. No. 1.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 AA; 76278 MW; 1F43A1F11919EF00 CRC64;
                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                 709 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE008334; AAR89915.1; -. HSSP; P02205; 1BDO.
GO; GO:0009524; F:ATF binding; IEA.
GO; GO:0009524; F:ATF binding; IEA.
GO; GO:0009152; P:Metebolism; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:001682; P:Metebolism; IEA.
InterPro; IPR001882; Biotin Garb C.
InterPro; IPR001882; Biotin Lipoyl.
InterPro; IPR00189; Biotin Lipoyl.
InterPro; IPR0019481; CPase J. N.
InterPro; IPR011053; Hybrid motif.
Pfam; PF02785; Biotin Carb C; IPR011054; Rudmit hyb_motif.
Pfam; PF02785; Biotin Carb C; IPPR0319; Biotin Lipoyl; I.
PROSITE; PS00188; Biotin Lipoyl; I.
PROSITE; PS00188; BIOTIN; I.
PROSITE; PS00186; CPSASE I; UNKNOWN I.
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                         OrderedLocusNames=AGR_L_2704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.v.,
Best Local 7; Conservative
                                63.6%;
                 72.0%;
    Ouery Match
Best Local Similarity 63.0.
Track Track Conservative
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304 AATAAARAIDY 314
                                                                                                        258 AATAAARAIDY 268
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASIAAARVLDY 11
                                                                            1 ASIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Cereon;
                                                                                                                                                                                                                                                           2704p
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SEQUENCE
                                                                                                                                                                                                7CSK5;
                                                                                                                                                                                    07CSK5
                                                                                                                                                     RESULT 8
Q7CSK5
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Gaps

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72.0%; Score 36; DB 2; Length 723; 80.0%; Pred. No. 1.9e+02; Live 1; Mismatches 1; Indels

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MEDLINE=22828297; PubMed=14500908; DOI=10.1073/pnas.1932838100;

MEDLINE=22828297; PubMed=14500908; DOI=10.1073/pnas.1932838100;

MADLINE=22828297; PubMed=14500908; DOI=10.1073/pnas.1932838100;

MADLINE=22828297; PubMed=14500908; DOI=10.1074/pnas.1932838100;

MADLINE=22828297; PubMed=14500908 A.; Keller H., Jagtap P., Linke B.,

MADLINE=22828297; PubMed=14500908 A.; Linke B.,

MADLINE=22828297; MADLINE=238283 A.; Linke B.,

MADLINE=22828297; PubMed=14500908; Linke B.,

MADLINE=228282999; Linke A.; Linke A.; Linke B.,

MADLINE=22828299; Linke A.; Linke A.; Linke B.; Linke A.; Linke B.; Linke A.; Linke B.; Linke
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                                                                                                                                                                                                                                     FLAGELIAR FUNCTIONAL PROTEIN.
Name=PFLA, OrderdocusNames=W50490;
Wolinella succinogenes.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; Flägellum.
SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;
                                                      Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|| |: ||
322 ASLAAVRLADY 332
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASIAAARVLDY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=844;
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RESULT 11 Q69X93

Created) Last sequence update) Last annotation update)

(TrEMBLrel. 23, (TrEMBLrel. 23, 1 (TrEMBLrel. 25, 1

01-MAR-2003 01-MAR-2003 01-OCT-2003

723 AA

PRELIMINARY;

Q8H034 Q8H034;

084034 ID 08 AC 08 DT 01 DT 01

RESULT 9

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Best Local Similarity 80.0 Matches 8; Conservative
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| AAIAAARVLN 108
                                                                                                                                                                                                                                                                                                                                                                                                       1 ASIAAARVL 9
||:||||||
7 ASLAAARVL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASIAAARVLD 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Li Submitted (MAY-2011) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
RMBL; AP00542; BAD32908.1; -.
RG GO; GO:0005524; F:AFP binding; IEA.
GO; GO:0004674; F:Protein-tyrosine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
RG; GO:0004872; F:receptor activity; IEA.
RG; GO:0004688; P:protein-tyrosine kinase activity; IEA.
RG; GO:0006468; P:protein-tyrosine kinase activity; IEA.
RINGEPRO; IPR00109; Kinase_like.
R InterPro; IPR001591; LRR_Lyp.
R InterPro; IPR001591; LRR_Lyp.
R InterPro; IPR002290; Ser_thr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF000560; LRR_L; Dkinase.
R Pfam; PF000569; Pkinase.
R Pfam; PF00059; Pkinase.
R PFAM; PF00069; Pkinase.
R PRINTS; PR00069; Pkinase.
                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Brkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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MEDILINE-94181269, PubMed=8134119;
Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
Frenkel N., Rosenthal L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; PRO0001; Proc kinase; 1.
SMART; SM00369; LRR TYP; 11.
SMART; SM00220; 2 TKc; 1.
SMART; SM002219; Tyrkc; 1.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; UNKNOWN_1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0633E08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 36; DB 2; Length 1072; 80.0%; Pred. No. 2.7e+02; live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1072 AA; 114368 MW; E15B809971B15F78 CRC64;
                                         Q69X93;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28; Last annotation update)
Putative receptor-like protein kinase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human herpesvírus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     069582 PRELIMINARY, PRT; 143 AA. 069582; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Herpesvirus Type 6 DNA.
                          1072 AA
                       PRT;
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 80.0
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SECRAIN=LSY54 / DSM 12343;
STRAIN=LSY54 / DSM 12343;
STRAIN=LSY54 / DSM 12343;
PubMedal5305914;
Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
Teeling H., Leuechner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
Klenk H.-P.,
"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
EMBL; CR522870; CAG35482.1;
EMBL; CR522870; CAG35482.1;
COMPLETE proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gарв
"A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates {\rm HIV-1."}_i, Oncogene 9:1167-1175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
NCBI_TaxID=84980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 70.0%; Score 35; DB 2; Length 143; Best Local Similarity 88.9%; Pred. No. 63; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 35; DB 2; Length 184; 80.0%; Pred. No. 81; tive 2; Mismatches 0; Indels
                                                                                                                                            [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Thompson J.T., Thompson J.T., Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases. EMBL; X73675; CAA22028.1; -. PIR; 843071; S43071. FIR; 843071; SA3071. FIR; SA3071; SA3071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6AQ91 PRELIMINARY; PRT; 184 AA. Q6AQ91; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Hypothetical protein. OrderedLocusNames=DP0753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9RJR7;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative zinc-binding oxidoreductase.
ORFNames=SCF51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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STRAIN=A3(2) / M145;
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098JR7
AC 098JRA
DT 01-MA
DT 01-MA
DT 01-MA
DT 08 Strep
CO STREP
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"Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevistae includes the mitochondrial ribosomal protein L8.";
Yeast 11:57-60(1995).
                                                                                                                                                                                                                                              GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA. GO:0008270; F:zinc ion binding; IEA. InterPro; IPR012085; Adh zn family. InterPro; IPR011032; GroES_like. Pfam; PF00107; AH_zinc_N; I.
             Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitech E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEE-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 44, Last annotation update)
Hypothetical 80.4 kDa protein in SMC3-MRRD4 intergenic region.
OrderedLocusNames=YJLO73W; ORFNames=J1083, HRC558;
Saccharomyces cerevisiae (Bakert).
Bukaryota; Fungi; Ascomycota; Saccharomycetas; Saccharomycetas; Saccharomycetales;
                                                                                                                                                    Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.0%; Score 35; DB 2; Length 329; Best Local Similarity 70.0%; Pred. No. 1.4e+02; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entian K.D.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
   MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                      329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;
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                                                                                                                                                                                  coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL, AL939105; CAB59716.1;
HSSP, Q8L3C8; 11YZ.
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Submitted (SEP-1995)
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SEQUENCE 329 AA;
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P40358;
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                                                                                                                              GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:000300; C:peripheral to membrane of membrane fraction; IDA.
GO; GO:0003767; F:co-chaperone activity; IGI.
GO; GO:0000742; P:karyogam during conjugation with cellular . . .; IGI.
GO; GO:000647; P:procein folding; IGI.
InterPro; IPR01623; DnaJ.N.
FRAM; PR0226; DnaJ. 1.
FRAM; PR021TE; PS00636; DNAJ. 1; FALSE_NEG.
PROSITE; PS00636; DNAJ. 2; 1.
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692 AA; 80381 MW; 9F612DD16B66981B CRC64;
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Job time : 75.2188 secs
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EMBL; X88851; CAA61312.1; -
EMBL; Z34288; CAA84049.1; -
PIR; S56849; S56849.
HSSP; D6622; BQZ.
GermOnline; 141687; -.
SGD; S000003609; JEM1.
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245 SLAAAIILDY 254
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                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
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Matches
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C007 T7:KC.OT C

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

model using sw protein search, OM protein

October 14, 2005, 15:51:19; Search time 99.9375 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-13 66 Title: Perfect score:

1 SGSTSNIGNNYVS 13 Sequence:

Scoring table:

2105692 seqs, 386760381 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp2190s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Adp45906 Human BLy Adg96733 Single ch Adg98729 Single ch Ade3872 Chemokine Abp45671 Human BLy Abp45917 Human BLy Abp45917 Human BLy Abp45917 Human BLy Abp45917 Human BLy Abp45918 Human BLy Abp4598 Human BLy Adg30413 Human BLy Adg30459 Human GMB Adg30458 Human GMB Adg30458 Single ch Adg96715 Single ch Adg96716 Single ch Adg96750 Single ch Adg96750 Single ch	Adg34304 Neurokini
5 ABP45906 7 ADG96733 8 ADG96729 8 ADG96729 5 ABP45672 5 ABP45923 5 ABP45923 5 ABP45917 7 ADG30413 7 ADG96749 7 ADG96750 7 ADG96750 7 ADG96750 7 ADG96750 8 ADG96750	• •
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45

ALIGNMENTS

RESULT 1 AAY79071

AAY79071 standard, peptide, 13 AA.

AAY79071;

(first entry) 12-JUN-2000

Anti-factor IX/IXa antibody L chain V domain CDR1 amino acid sequence

Complementarity determining region 1; CDR1; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary arter; bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

ä Kirchhofer Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serime protease that participates in the blood coaqulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

Sequence 109 AA;

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies binding specifically to detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte sample. The antibodies can be used as an alternative means of treatment for obese the antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies
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              the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metastasis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular cosgulopathy (DIC)
platelets. Compositions comprising the antibodies are used for
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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; Pred. No. 0.00029;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02544 standard; protein; 109 AA.
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                                                                                                                                                                                                                                                                  100.0%;
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Matches 13; Conservative
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can be used as a therapeutic itself. Autibodise binding specifically to chestry to the antibodises of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and cobsenty related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used to activate the immune system to destroy the cells of complement mediated lysis. The antibodies binding specifically to detectable label such as radiolabel, fluorescent or chemical group and cectable label such as radiolabel, fluorescent or chemical group and cectable label such as radiolabel, fluorescent or detection and electron methods of diagnosis in human subjects e.g. to detect or detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
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llarity 100.0%; Pred. No. 0.0026;
Conservative 0; Mismatches 0; Indels
100.0%; Score 66; DB 4; Length 109; 100.0%; Pred. No. 0.0026; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            Anti-adipocyte monoclonal antibody light chain, FAT 44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 128-129; 182pp; English
                                                                                                                                                                                                                    AAU02558 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2000; 2000WO-GB003900.
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                                                                                1 SGSTSNIGNNYVS 13
                                            13; Conservative
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les 13; Conserva
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      Query Match
Best Local Similarity
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AAU02627 standard; protein; 110 AA

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23 SGSTSNIGNNYVS 35
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AAU02612 standard; protein; 110 AA AAU02612;

(first entry)

Anti-adipocyte monoclonal antibody light chain, FAT 99.

Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

Homo sapiens

WO200127279-A1

19-APR-2001

11-OCT-2000; 2000WO-GB003900;

12-OCT-1999;

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Vaughan TJ; Edwards BM, Main SH,

WPI; 2001-282031/29. N-PSDB; AAS03512.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 163; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
besity related diseases. The antibodies can be used to deliver drugs or
prodrugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
caplement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
cativate an be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease

Sequence 110 AA;

Gaps ö 100.0%; Score 66; DB 4; Length 110; 100.0%; Pred. No. 0.0026; Ative 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity

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1 SGSTSNIGNNYVS 13 SGSTSNIGNNYVS 35

RESULT 5 AAU02627

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
cobesity related diseases. The antibodies can be used to deliver drugs or
con be used as therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
confidence of adipocyte artigonals in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
confinence than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intraconfinence. Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related Gaps ö fat; 100.0%; Score 66; DB 4; Length 110; 100.0%; Pred. No. 0.0026; Pred. o; Mismatches 0; Indels Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR. Anti-adipocyte monoclonal antibody light chain, FAT 112. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. Claim 1; Page 172; 182pp; English. 11-OCT-2000; 2000WO-GB003900. 12-OCT-1999; 99US-0158812P (first entry) 23 SGSTSNIGNNYVS 35 1 SGSTSNIGNNYVS 13 13; Conservative Main SH, WPI; 2001-282031/29. Best Local Similarity Matches 13; Conserv N-PSDB; AAS03527 Sequence 110 AA; WO200127279-A1. Homo sapiens. 29-AUG-2001 Edwarde BM, 19-APR-2001 diseases Query Match ઠે

Anti-adipocyte monoclonal antibody light chain, FAT 113. AAU02629 standard; protein; 110 AA. (first entry) 29-AUG-2001 AAU02629; RESULT 6
AAU02629
ID AAU0
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
cobesity related diseases. The antibodies can be used to deliver drugs or
con be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis in human subjects e.g. to determine the
consed in methods of diagnosis in human subjects e.g. to determine the
consence of adipocyte antigen on the surface of an adipocyte of detect or
determine the presence or level of adipocytes in a cell or tissue sample.
Constitution of the used as an alternative means of treatment for obese
constitution of the than undergoing surgery to remove excess fat. Antibodies
constitutional fat associated with heart disease
                                                                                                                                                                                                                                                                                      Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                   CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 118-119; 182pp; English.
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                  11-OCT-2000; 2000WO-GB003900.
                                                                    99US-0158812P.
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                                                                                                                                                                     Edwards BM, Main SH,
                                                                                                                                                                                                                         WPI; 2001-282031/29
                                                                                                                                                                                                                                                   N-PSDB; AAS03442
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                                                                    12-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
chesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
creatible label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
creatible label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
creatible label such as radiolabel, fluorescent or thesuse sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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100.0%; Pred. No. 0.0026;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 173; 182pp; English
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Best Local Similarity 100.
Matches 13; Conservative
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N-PSDB; AAS03529.
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                                                                                                                                WO200127279-A1
                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                   12-OCT-1999;
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Gaps

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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Vaughan TJ;

Main SH,

Edwards BM,

WO200127279-A1

19-APR-2001

Homo sapiens

BXBXGXXXXXX

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WPI; 2001-282031/29. N-PSDB; AAS03451.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 124; 182pp; English.

ANU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
consists related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding apecifically to
caption of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease

Sequence 111 AA;

Gaps ô 100.0%; Score 66; DB 4; Length 111; 100.0%; Pred. No. 0.0027; Pred. No. 0, Mismatches 0; Indels Best Local Similarity 100. Matches 13; Conservative

24 SGSTSNIGNNYVS 36

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ABP45887;

Homo sapiens

10-JAN-2002

15-JUN-2001; 2001WO-US019110.

1 SGSTSNIGNNYVS 13 ઠ

ABP45887 standard; protein; 240 AA. 19-AUG-2002 (first entry) RESULT 9 ABP45887

Human BLyS binding scFv SEQ ID 1898.

BLy8; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiALDS; vaccine; cancer; immune; auttoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

WO200202641-A1.

16-JUN-2000; 2000US-0212210P. 17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-0276248P. 21-WAR-2001; 2001US-0293499P.

HUMAN GENOME SCI INC. CAMBRIDGE ANTIBODY TECHNOLOGY. (HUMA-) (CAMB-)

Vaughan T, Choi GH, Barash SC, WPI; 2002-114799/15. Ruben SM,

Hilbert D;

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2666-2667; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antithemmatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

Sequence 240 AA;

Gape ö Length 240; 100.0%; Score 66; DB 5; Length 24 100.0%; Pred. No. 0.0059; ive 0; Mismatches 0; Indele Query Match
Best Local Similarity 100.
Matches 13; Conservative

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ADG96714 standard; protein; 240 AA.

ADG96714;

(first entry) 11-MAR-2004

Single chain antibody that immunospecifically binds BLyS SeqID 1898

antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.

Unidentified

402003055979-A2.

10-JUL-2003.

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC

Choi GH, Vaughan TJ, Hilbert D; Ruben SM, Barash SC,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g.

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to thromosome 1944 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The fragment thereof, of either human, murine, rat or monkey BLyS. The fragment invention refers to the use of such antibodies in various methods of present invention refers to the use of such antibodies in various methods contraint expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysethenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and cortivities such as antirheumatic, antiallergic and cytostatic. This activities such as antirheumatic, antiallergic and cytostatic. This colypeptide sequence date for this patent did not form part of the printed specification, but was obtained in electronic format contractly from WIPO at ftp.wipo.int/published pott_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 66; DB 7; Length 240; 100.0%; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
rheumatoid arthritis, asthma and leukemia.
                                    Example 1; SEQ ID NO 1898; 394pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurokinin B antibody SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG34301 standard; protein; 242 AA
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Best Local Similarity 100.
Matches 13; Conservative
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N-PSDB; ADG34282.
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The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preclampsia. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody that specifically binds neurokinin B, useful for preparing composition for treating or preventing hypertension or preeclampsia.
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                                                                                                                                          100.0%; Score 66; DB 8; Length 242;
100.0%; Pred. No. 0.006;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                  ADG34317 standard; protein; 242 AA.
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Best Local Similarity
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                                                                                                                  Sequence 242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                      invention.
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0; Indels

RESULT 13 ABP45916

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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomdulatory; antirheumatic; antiALDS; vaccine; cancer; immune; auttoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                  Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2700-2701; 3148pp; English.
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                     Human BLyS binding scFv SEQ ID 1927
    ABP45916 standard; protein; 243 AA.
                                                                                                                                                                                                                                                               16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0293499P.
                                                                                                                                                                                                                                           15-JUN-2001; 2001WO-US019110.
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-114799/15.
                                                                                                                                                                                              WO200202641-A1
                                                                                                                                                                         Homo sapiens
                                                 19-AUG-2002
                                                                                                                                                                                                                     10-JAN-2002
                          ABP45916;
```

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the E Lymphocyte Stimulator (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory.

C of thibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant bLyS expression and activity such as cancer, immune, and autoimmune disorders and cliebases.

C administered to go enemon variable immunosficiency (VID) and climunodeficiency (e.g. common variable immunosficiency (VID) and committed in the common variable immunosficiency (VID) and common variable immunosficiency (VID) and committed in the common variable immunosficiency (VID) and committed variable immunosficiency (VID) and committed variable immunosficiency (VID) and committed variable variable variable variable variable variable variable uired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent antibodies and fragments of the antibodies described in the method of acquired

Sequence 243 AA;

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Gaps
                                              ö
     100.0%; Score 66; DB 5; Length 243; 100.0%; Pred. No. 0.006; 1. Indels ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
Matches 13; Conservative
```

RESULT 14

AAO31147 standard; protein; 243 AA AAO31147 ID AAO3

```
Human; protein coordinate data; heavy chain variable domain; VH; cancer; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TRY; tumour necrosis factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL related apoptosis-inducing ligand; KRaposi, R sarcoma; central nervous system; medulloblastoma; neuroblastoma; glioblastoma; antibody therapy; nootropic; ALDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; antibody.
                                                   Human CM085C11 scFv protein that specifically binds TR7
                                                                                                                                                                                                                                                            ; 2002US-0369877P.
; 2002US-0384828P.
; 2002US-0396591P.
                                                                                                                                                                                                                                19-DEC-2002; 2002WO-US040597.
                                                                                                                                                                                                                                                                                 18-JUL-2002; 2002US-0396591P.
15-AUG-2002; 2002US-0403370P.
13-NOV-2002; 2002US-0425737P.
                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                             06-OCT-2003 (first entry)
                                                                                                                                                                                       WO2003054216-A2.
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                              05-APR-2002;
04-JUN-2002;
                                                                                                                                                                                                            03-JUL-2003
```

Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;

Hilbert

WPI; 2003-569250/53. N-PSDB; AAL62844

lung New antibody or its fragment, useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lurgastrointestinal cancer, or Kaposi's sarcoma or, graft versus host disease, AIDS

Claim 2; Page 288; 301pp; English.

WHCDR1 (heavy chain variable domain complementarity determining region), WHCDR2, WHCDR3, WLCDR1 (light chain variable domain complementarity determining region), WLCDR2 or WLCDR3. The antibody or its fragment immunospecifically binds TRAIL (tumour necrosis factor; TWP-related apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or amtibody or its fragment is useful for treating, preventing or gastrointestinal cancer or Kaposi's sarcoma or cancer of the central nervous system such as medulloblastoma, neuroblastoma or gioblastoma or graft versus host disease, AIDS (acquired immune deficiency syndrome) or graft versus host disease, AIDS (acquired immune deficiency syndrome) or neurodegenerative disorder. The invention is useful in antibody nerapy. The present sequence is human scFv protein that specifically The invention relates to an isolated antibody or its fragments such

Sequence 243 AA;

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Gape
                                 ö
100.0%; Score 66; DB 6; Length 243; 100.0%; Pred. No. 0.006; 1.1ve 0; Mismatches 0; Indels
              Local Similarity 100.
Query Match
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, thase compositions are useful for identifying immune disorders uncluding mysathenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and prodnosed including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antiashmatic, antiarthritic, neuroprotective, antiinflammatory, antiashmatic, antiallergic and cycostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the inventors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                       Single chain antibody that immunospecifically binds BLyS SeqID 1927.
                                                                                                                                                                                antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthania gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiathritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directely from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaughan TJ, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 1927; 394pp; English
               ADG96743 standard; protein; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2002; 2002WO-US036496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-505530/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 243 AA;
                                                                                                                                                                                                                                                                                                                                                                  WO2003055979-A2
                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                   11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2003
                                                            ADG96743;
ADG96743
```

Query Match
Best Local Similarity 100.0%; Pred. No. 0.006;
Bast Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 8

Search completed: October 14, 2005, 16:12:41

Job time : 100.938 secs

```
5 16:39:21 2005
Mon Dec
```

October 14, 2005, 16:00:04; Search time 25.5938 Seconds (without alignments) 37.917 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. - protein search, using sw model Title: Perfect score: Sequence: OM protein Run on:

US-10-614-959-13 66

1 SGSTSNIGNNYVS 13 Scoring table:

513545 segs, 74649064 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appli	Appli	loo!	Appli	Appli	Appli	(pp)	Appli
Ę	13,	37.	37.	36,	42,	43,	35,	36,	42,	43	39.	31,	18	39.	18	18	18,	62,	4		5.	4	. 4			7	7.
Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence			Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence
	09-383-667-13	-665-202-37	US-09-315-574-37	08-665-202-36	565-202-42	565-202-43	983-607-35	315-574-36	-315-574-42	09-315-574-43	565-202-39	US-08-983-607-31	JS-09-025-769B-18	315-574-39	US-09-490-070A-18	-490-153-18	US-09-490-324-18	240-274-62	372-425A-4	565-202-5	115-574-5	069-821-4	JS-09-956-086-4	JS-09-956-087-4	120-592A-7	185-442-7	US-09-983-580-7
A	-60-Sn	US-08-	-60-SD	US-08-	US-08-665-	US-08-665	US-08-983-	-60	8	US-09-	US-08-665-	US-08-	NS-09-(US-09-315-	US-09-4	ns-09-4	US-09-4	US-09-240-	ns-09-	US-08-665-	US-09-315-	-690-60-SN	5-60-SD	0S-09-5	US-09-420-5	US-09-985-4	5-60-SN
DB	4	~	4	7	~	N	m	4	4	4	~	m	ო	4	4	4	4	ო	4	N	4	n	4	4	m	4	4
Query Match Length	13	98	98	111	111	111	111	111	111	111	112	112	112	112	112	112	112	114	234	258	258	262	262	262	282	282	282
& Query Match	100.0	93.9	93.9	m	93.9	n		93.9	ω.	m.	93.9	ë.	•	•		93.9					93.9	93.9	٠	93.9	93.9	93.9	93.9
Score	99	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62
Result No.	1	7	m	4	C)	9	7	00	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27

Sequence 15, Appl	Sequence 40, Appl	Sequence 40. Appl	Sequence 112. App	55.	Sequence 32, Appl	Seguence 51. Appl	Sequence 32, Appl	Sequence 51. Appl	Sequence 32. Appl			Sequence 51, Appl	2	111	~	3	Sequence 59, Appl	
US-08-652-816A-15	US-08-665-202-40	US-09-315-574-40	US-08-211-202-112	US-09-240-274-55	US-09-025-769B-32	US-09-025-769B-51	US-09-490-070A-32	US-09-490-070A-51	US-09-490-153-32	US-09-490-153-51	US-09-490-324-32	US-09-490-324-51	US-08-199-911-2	US-08-211-202-111	US-08-665-202-38	US-09-315-574-38	US-09-240-274-59	
•	•	111 4	113 1	109	109 3	109 3	4 60	.09	.09 4	.09 4	.09	109 4	10 1	98 1	98 2	98 4	.09	
61 92.4 1	87.9	87.9	87.9	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4		83.3	80.3	80.3	53 80.3	53 80.3 1	
28	59	30	31	32	33	34	32.	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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### Sequence 37, Application US/08665202

### Sequence 37, Application US/086665202

### Sequence 37, Application 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sequence 13, Application US/0938367

Sequence 13, Application US/0938367

GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Bevanx, Brigitte
APPLICANT: Bevanx, Brigitte
APPLICANT: Bas, Philip E.
APPLICANT: Suggett, Bnile
APPLICANT: Suggett, Bnile
APPLICANT: Suggett, Bnile
APPLICANT: Wirchhofer, Daniel
APPLICANT: Suggett, Shelle
APPLICANT: Brerkence: Ple61R2
CURRENT APPLICANTON: Human Anti-Factor IX/IXa Antibodies
FILE REFRENCE: Ple61R2
CURRENT APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER PILING DATE: 1999-08-26
EARLIER PILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 32

LENGTH: 13

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SGSTSNIGNNYVS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-383-667-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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US 60/000,250
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

93.9%;

Best Local Similarity 92.3%;

Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 111 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-315-574-37
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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; Sequence 37, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marke, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: Tumor Antigens
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 0.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                COUNTRY: USA
ZIP: 94111-3814
ZIP: 94111-3816
ZIP: 94111-3816
ZIP: 94111-3816
ZIP: 94111-3816
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER: US/08/2307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
COMMUNICATION OCIDS
COMMUNICATION: ACIDS
COMMUNICATION OCIDS
COMMU
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COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%;
92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
              California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-665-202-37
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US-08-665-202-36

US-08-665-202-36

Sequence 36, Application US/08665202

Patent No. 5977322

APPLICANT: Marks, James D.
APPLICANT: Schier, Robert

TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCE: 141

CORRESPONDENCE: 141

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

CONTREY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 4; Length 98;
Pred. No. 0.007;
1; Mismatches 0; Indels
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUW TYPE: F10ppy disk
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 130 VORES
COMPUTER: 130 VORES
COMPUTER: 130 VORES
FILING DATE: 14-JUN-1996
FILING DATE: 14-JUN-1995
ATTING DATE: 15-JUN-1995

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
ATTORNEY/AGENT INFORMATION:
NAME: HULTHC., Tom
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATIC (415) 576-0200
TELEPRATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTENISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
```

Sequence 43, Application US/08665202

Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: Tumor Antigens

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

```
RESULT 5
US-08-665-202-42
i Sequence 42, Application US/08665202
i Sequence 42, Application US/08665202
i Patent No. 5977322
i GENERAL INFORMATION:
APPLICANT: MARKS, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to NUMBER OF SEQUENCES:
I CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                 Score 62; DB 2; Length 111;
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUDNIKT: USA

CUNTRY: USA

CUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FLING DATE: 13-UNN-1996
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FLING DATE: 14-UNN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FLING DATE: 15-UNN-1995
ATTORNEY/AGRAT INFORMATION:
NAME: HUNTEY, TOM
REGISTRATION NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBENOUS: (415) 576-0200
                                                                                                                                                                                    1; Mismatches
                                                                                                                              Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                  23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                 1 SGSTSNIGNNYVS 13
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-665-202-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                            g
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM

NAME: Hunter, Tom REGISTRATION NUMBER: 38,498 REFERENCE/DOCKET NUMBER: 02307E-061410 TELECOMMUNICATION INFORMATION:

, MOLECULE TYPE: peptide US-08-665-202-43 STRANDEDNESS:

ö Gaps Score 62; DB 2; Length 111; Pred. No. 0.0079; 1; Mismatches 0; Indels Sequence 35, Application US/08983607

Patent No. 6140470

GENERAL INPORMATION:

APPLICANT: Alan Garen

APPLICANT: Alan Garen

TITLE OF INVENTION: Human Anti-Tumor Monoclonal AntiTITLE OF INVENTION: bodies

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Department of Molecular Biophysics

ADDRESSEE: and Biochemistry, Yale University

STREET: 266 Whitney Avenue CITY: New macure STATE: Connecticut COUNTRY: United States of America ZIP: 06520-8114 93.9%; 92.3%; 1 SGSTSNIGNNYVS 13 Query Match Best Local Similarity 92.3 Matches 12; Conservative

Length 111;

Score 62, DB 2; Length 111 Pred. No. 0.0079; 1; Mismatches 0; Indels

93.9%;

Best Local Similarity 92.3 Matches 12; Conservative

RESULT 6 US-08-665-202-43

```
CLASSIFICATION: 5.0.

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE: 14-JUN.1995

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 13, 498

REFERENCE/DOCKET NUMBER: 38, 498

REFERENCE/DOCKET NUMBER: 38, 498

REFERENCE/DOCKET NUMBER: 38, 576.030

TELECOMUNICATION INFORMATION:

TELEPHONE: (415) 576.0300

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

STRANDEDNESS:

TYPE: amino acid

STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.9%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SGSSSNIGNNYVS 35
20-MAY-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-315-574-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%; Score 62; DB 3; Length 111; 92.3%; Pred. No. 0.0079; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens (melanoma patient immu-ORGANISM: nized with autologous tumor cells) INDIVIDUAL ISOLATE: peripheral blood lymphocytes IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: DM414 scFv antibodies obtained from LIBRARY: fUSE5 fusion phage construct
                                  COMPUTER: IBW PC
OPERATING SYSTEM: MS DOS
SOOFWARE: WORD PROCESSING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION WHERE: PCT/1B96/01032
FILING DATE: JUNE 28, 1996
CLASSIFICATION: 435
ATTORNEY, AGENT INPREMENTION:
NAME: MATY M: KTINEKY
REFERENCE DOCKEY NUMBER: 32423
REFERENCE DOCKEY NUMBER: 32423
REFERENCE DOCKEY NUMBER: 0CR-679
TELECHONE: 203-773-1183
INFORMATION FOR SEG ID NO: 35:
SEQUENCE CHARACTERISTICS:
TEMMOTH: 111 residues
        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.9
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-09-315-574-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-983-607-35
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Sequence 42, Application US/09315574

Patent No. 6512097

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: APPLICANT: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS: Appendix Pour Embarcadero Center, Suite 1100
CITY: San Francisco
STREET: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                         Length 111;
                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: CALL COUNTRY

ZIP: 94111-4106

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICANTON: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
FILING DATE: 11-JUN-1995
FILING DATE: 11-JUN-1996
ATTORNEY AGENT INFORMATION:
NAME: HUNTER, TOM
                                                                                                                                                                                                                                                                                                              Score 62; DB 4;
Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
02307E-061411
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REGISTRATION NUMBER: 38,498
REPERBENGE/DOCKET NUMBER: 02307E-061411
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
COO7 T7:65:0T C
                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-42
בוכל
בוכל
בוכל
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Gaps ö Score 62; DB 4; Length 111; Pred. No. 0.0079; 1; Mismatches 0; Indels 93.9%; 92.3%; 23 SGSSSNIGNNYVS 35 Query Match Best Local Similarity 92.3 Matches 12; Conservative 1 SGSTSNIGNNYVS 13 ઠ 셤

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Sequence 43, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS: RESULT 10 US-09-315-574-43

ADDRESSE:
ADDRESSE:
ADDRESSE:
STRET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SCTARARS PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY -99
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
ATTOMNEY/AGENT INFORMATION:
ANAME: ALCORMATION:
ANA

NAME: Hunter, Tom REGISTRATION NUMBER: 38,498 REFERENCE/DOCKET NUMBER: 02307E-061411 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:

| LENGTH: 111 amino acids | TYPE: amino acid | STRANDEDNESS: | TOPOLOGY: linear | MOLECULE TYPE: peptide | US-09-315-574-43

Sequence 39, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
STREET: San Francisco
STREET: California Gaps ô Length 111; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATTORNEY AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REPERBENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 39:

SEQUENCE CHARACTERISTICS: Score 62; DB 4; Pred. No. 0.0079; 1; Mismatches 0 Query Match 93.9%; Best Local Similarity 92.3%; Matches 12; Conservative 1 SGSTSNIGNNYVS 13 23 SGSSSNIGNNYVS 35 LENGTH: 112 amino acids MOLECULE TYPE: peptide TOPOLOGY: linear RESULT 11 US-08-665-202-39 COUNTRY: ઠે

Score 62, DB 2; Length 112; Pred. No. 0.008; 1; Mismatches 0; Indels Query Match
Best Local Similarity 92.3' 1 SGSTSNIGNNYVS 13 23 SGSSSNIGNNYVS 35 ð

93.9%; 92.3%;

US-08-665-202-39

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RESULT 12
US-08-983-607-31
US-08-983-607-31
; Sequence 11, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
APPLICANT: Alan Garen

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COMPUTE TOUZI
COMPUTE TOUZI
COMPUTE TOUZI
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-199
PRIOR APPLICATION UNMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (2215)96-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 112;
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 3;
Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 112 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 SGSSSNIGNNYVS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-025-769B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                            CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                              10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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  APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES:
ADDRESSE: 51
CORRESPONDENCE ADDRES:
ADDRESSE: and Biochemistry, Yale University
STREET: Connecticut
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER: D6520-8114
COMPUTER: BLADABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: Word Processing
COMPUTER: Word Processing
COMPUTER: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: ADTI 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
PILING DATE: JUNE 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: 32423
REFERENCE/DOCKET NUMBER: 323-33
INFORMATION FOR SEQ ID NO: 31:
SEGUENCE CHARACTER/ESTICS:
LEMMATIN FOR SEQ ID NO: 31:
SEGUENCE CHARACTER/ESTICS:
LEMMATH 112 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STOP-0257693 Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Raspik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Procept Simon
APPLICANT: Plackthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: DM414 BCFv antibodies obtained from LIBRARY: _fUSE5 fusion phage construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 3;
Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: polypeptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 SGSSSNIGNNYVS 36
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US-08-983-607-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 112 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-025-769B-18
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Gaps

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Indels

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US-09-315-574-39

US-09-315-574-39

US-09-315-574-39

Sequence 39, Application US/09315574

Sequence 39, Application US/09315574

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.

STREET: Pour Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION 1530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
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Page 7
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us-10-614-959-13.rai

E007 T7:65:0T C

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PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 60/000,250

PRIOR DATE: 15-7UN-1995

PRIOR APPLICATION DATA:

APPLICATION DATA:

PILING DATE: 13-7UN-1996

FILING DATE: 13-7UN-1996

ATTORNEY AGENT INFORMATION:

NAME: HUNTER, TOM

REFERENCE/DOCKET NUMBER: 02307E-061411

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300

TELEPAX: (415) 576-0300

TELEPAX: (415) 576-0300

TELEPAX: (415) 576-0300

TELEPAX: (415) 276-0300

TELEPAX: (415) 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOSY: linear

MOLECULE TYPE: peptide

US-09-315-574-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 373
CORRESPONDENCE S. 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
Mhite & McAuliffe

STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2006
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENAPPY disk
COMPUTER: ENAPPY disk
COMPUTER: ENAPPE: Floppy disk
COMPUTER: ENAPPE: Ploppy disk
COMPUTER: ENAPPY disk
COMPUTER: ENAPPY disk
COMPUTER: ENAPPY disk
COMPUTER: ENAPPY disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
FILING DATE: 18-Aug-1200
FILING DATE: 18-Aug-1200
FILING DATE: 18-Aug-1995
ATTORNEY/AGRIT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/POCKET NUMBER: 31,298
REFERENCE/POCKET NUMBER: 31,298
REFERENCE/POCKET NUMBER: 31,200
TELEPAM: (202) 912-200
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                     ö
  Score 62; DB 4; Length 112;
Pred. No. 0.008;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            RESULT 15
US-09-490-070A-18
Sequence 18, Application US/09490070A
Patent No. 656548
GENERAL INFORMATION:
Pack, Peter
Ilag, Vic
Query Match 93.9%;
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                    23 SGSSSNIGNNYVS 35
                                                                                              1 SGSTSNIGNNYVS 13
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October 14, 2005, 16:20:10 ; Search time 92.4219 Seconds (without alignments) 58.615 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                            OM protein - protein search, using sw model
                                                                                                                                             Run on:
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US-10-614-959-13 66 Title: Perfect score:

1 SGSTSNIGNNYVS 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1859788 seqs, 416717961 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	mence 1898. An	The 1898 An	Semience 24 Appl	mence 40 Appl	mence 1927 An	Tacinco 1327, Ap	mence 1927 Appr	mence 29 Appl	mence 22, Appl	nence 33, Appr	יייייייייייייייייייייייייייייייייייייי
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DB]		15				14		18		18	
Query Match Length	240	240	242	242	243	243	243	243	243	243	27.2
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100
Score	99	99	99	99	99	99	99	99	99	99	9
Result No.	1	7	m	4	2	9	7	80	o,	10	-

Sequence 53. Appl	23	equence 26.	equence 192	equence 1926	equence 3241.	equence 31,	equence 36,	equence 191	e 191	e 191	191	1443	equence 1682	equence 1707	189	e 1928	1934	equence 144	1682	quence 1707	1899	1926	1934	46,	98	equence 27,	3 37,	9 44	e 39,	e 1419	1618	equence 2049	e 141
-673-5	-10-981-691-	0-981-692-2	-09-880-748-192	-10-293-418-1	93-418-324	-10-981-692-3	-692-3	-09-880-748-191	-09-880-1	-10 - 293 - 418 - 1	-10-293-418-191	09-880-748-144	-60	-09-880-748-170	-09-880-748-189	-09-880-748-192	-09-880-748-193	-10-293-418-144	-10-293-418-168	-10-293-418-17	-10-293-418-189	-10-293-418-192	-10-293-418-19	-10-935-290-4	-10-935-290-8	-10-981-692-2	-10-981-69	US-11-046-857-44	-10-981-	-09-880-748-141	-09-880-748-161	-09-880-748-20	
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243	243	244	245	245	245	245	245	246	246	246	246	247	247	247	247	247	247	247	247	247	247	247	247	247	247	247	247	247	248	249	249	249	249
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ALIGNMENTS

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Sequence 1898, Application US/0980748
; Sequence 1898, Application US/0980748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; CURRENT PAPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR PILING DATE: 2000-06-15
; PRIOR PILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-16
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-25
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898
US-09-880-748-1898
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Query Match
100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (1 SGSTSNIGNNYVS 13

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Gaps

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0; Mismatches
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; OTHER INFORMATION: NOISDIO SCFV US-10-981-692-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 SGSTSNIGNNYVS 167
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                                       154 SGSTSNIGNNYVS 166
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Best Local Similarity 100.
Matches 13; Conservative
1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-880-748-1927
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Sequence 24, Application US/10981692

Publication No. US2005016377A1

GENERAL INFORMATION:

TITLE OF INVENTION: Altibodies that Specifically Bind to Neurokinin B

TITLE OF INVENTION: Altibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PF590P1

CURRENT FILING DATE: 2004-11-05

PRIOR PILING DATE: 2005-29

PRIOR APPLICATION NUMBER: 6C/383,802

PRIOR PILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 24

LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                   Sequence 1899, Application US/10293418

Sequence 1899, Application No. US20030223996A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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Best Local Similarity 100.0%; Score 66; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 66; DB 15; Length 240; 100.0%; Pred. No. 0.007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: NO15E08 scFv US-10-981-692-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 SGSTSNIGNNYVS 165
         153 SGSTSNIGNNYVS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-293-418-1898
                                                                                                US-10-293-418-1898
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-10-981-692-24
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Sequence 40. Application US/10981692
; Sequence 40. Application No. US2005016377A1
; Dublication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT Rosen et al.
; TITLE ON INVENTION: Antibodies that Specifically Bind to Neurokinin B
; TITLE REFERENCE: PF590P1
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2005-29
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
LUNGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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US-09-880-748-1927

US-09-880-748-1927

Sequence 1927, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5.3

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT ELLING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PRECENTIN VET. 2.0

SEQ ID NO 1927
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; ORGANISM: Homo Bapiens
US-10-293-418-1927
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                                                                                                                                Sequence 53, Application US/10322673

Publication No. US20030180296A1

GENERAL INFORMATION:

APPLICANT: Salcede et al.

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF585

CURRENT PILING DATE: 2002-12-19

FRIOR APPLICATION NUMBER: 60/341,237

FRIOR APPLICATION NUMBER: 60/344,828

FRIOR PILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-01-18

PRIOR FILING DATE: 2002-11-13

SEQ ID NO 53

LENGTH: 243
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Fublication No. US20030223996A1
GENERAL INPORMATION:
APPLICART: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF52782
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-17
PRIOR PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PRIOR PRIOR DATE: 2000-10-17
PRIOR PRIOR PRIING DATE: 2000-10-17
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 
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100.0%; Score 66; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
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ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                        ## Sequence 29, Application US/10981692
## Sequence 29, Application US/10981692
## Publication No. US20050163777A1
## GENERAL INFORMATION:
## APPLICANT: Rosen et al.
## TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
## FILE REFERENCE: PF590P1
## CURRENT APPLICATION NUMBER: US/10/981,692
## CURRENT APPLICATION NUMBER: PCT/US03/16802
## PRIOR APPLICATION NUMBER: 60/383,802
## PRIOR FILING DATE: 2003-05-30
## PRIOR FILING DATE: 2002-05-30
## PRIOR FILING DATE: 2002-05-30
## SOFTWARE: Patentin version 3.1
## SEQ ID NO 29
## LENGTH: 243
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US-10-981-692-33

i Sequence 33, Application US/10981692

publication No. US20050163777A1

GENERAL INFORMATION:

A TAPLICAMY: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PF590P1

CURRENT FILING DATE: 2004-11-05

PRIOR APPLICATION NUMBER: PC7/US03/16802

PRIOR APPLICATION NUMBER: 60/383,802

PRIOR PILING DATE: 2003-05-29

PRIOR PILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SEQ ID NOS: 76

SEQ ID NO 33

LENGTH: 243
                                                        Gaps
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Query Match
100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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US-10-981-692-29
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CTHER INFORMATION: N023E01 BCFV

US-10-981-692-33
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ORGANISM: Artificial sequence
FEATURE:
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US-10-981-692-29
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, OTHER INFORMATION: CM085C11 8CFV US-10-981-673-53
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; OTHER INFORMATION: CM085C11 SCFV
US-10-981-621-53
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ORGANISM: Artificial sequence
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; Sequence 53. Application US/10981621
; Publication No. US20050214206A1
; Publication No. US20050214206A1
; GENERAL INFORMATION:
    APPLICAMY: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
    FILE REFERENCE: PF568FD11
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2004-09-10
; PRIOR FILING DATE: 2004-09-10
; PRIOR FILING DATE: 2004-05-05
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
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US-10-981-465-30
US-10-981-465-30
US-10-981-465-30
US-10-981-465-30
US-10-981-465-30
US-10-981-165-30
US-10-981-165-30
US-10-981-165-30
US-10-981-165-30
US-10-981-160

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100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
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RESULT 12
US-10-981-673-53

FRESULT 12
Sequence 53, Application US/10981673

Sequence 53, Application World Sequence 53, Application No. US20050214207A1

GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF885P1D2
CURRENT FILING DATE: 2004-11-05
PRIOR FILING DATE: 2004-11-05
PRIOR FILING DATE: 2004-05-10
PRIOR FILING DATE: 2004-05-10
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
PRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2002-06-04
PRIOR FILING DATE: 2002-07-18
PRIOR PRIOR PAPICATION NUMBER: 60/425, 737
PRIOR PRIOR PAPICATION NUMBER: 60/425, 737
PRIOR PAPICATION NUMBER: 60/425, 737
PRIOR PAPICATION NUMBER: 60/425, 737
PRIOR PAPICATION NUMBER: 60/425, 737
PRIOR PAPICATION NUMBER: 60/425, 737
PRIOR PAPICATION NUMBER: 60/426, 737
PRIOR FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: 10/322,673
PRIOR PELICATION NUMBER: 10/322,673
PRIOR PILING DATE: 2002-12-19
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-06-04
PRIOR PILING DATE: 2002-06-15
PRIOR PILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 53
LENGTH: 243
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Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels
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RESULT 18

US-10-981-691-53

US-10-981-691-53

Sequence 53, Application US/10981691

Publicacion No. US20050214208A1

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Receptors

FILE REFERENCE: PFS85P1D3

CURRENT APPLICATION NUMBER: US/10/981,691

CURRENT APPLICATION NUMBER: US/10/981,691

CURRENT FILING DATE: 2004-09-10-05

PRIOR FILING DATE: 2004-05-05

PRIOR FILING DATE: 2004-05-05

PRIOR FILING DATE: 2003-05-06

PRIOR FILING DATE: 2003-06-140

PRIOR FILING DATE: 2002-04-05

PRIOR PRILING DATE: 2002-04-05

PRIOR PILING DATE:
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Query Match
100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels (
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COTHER INFORMATION: CM085C11 BCFV

US-10-981-691-53
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ö Gaps ö 100.0%; Score 66; DB 18; Length 243; 100.0%; Pred. No. 0.007; tive 0; Mismatches 0; Indels (Query Match
Best Local Similarity 100.
Matches 13; Conservative

1 SGSTSNIGNNYVS 13

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155 SGSTSNIGNNYVS 167

US-10-981-692-26
Sequence 26, Application US/10981692
Sequence 26, Application US/10981692
Sequence 26, Application US/10981692
Sequence 26, Application US/10981692
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B CURRENT APPLICATION NUMBER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/USO3/16802
PRIOR FILING DATE: 2003-05-29
PRIOR PRILING DATE: 2003-05-30

Gape Sequence 1926, Application US/0980748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR PRIOR DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PeatentIn Ver. 2.0 ö Query Match 100.0%; Score 66; DB 18; Length 244; Best Local Similarity 100.0%; Pred. No. 0.0071; Matches 13; Conservative 0; Mismatches 0; Indels (100.0%; Score 66; DB 10; Length 245; 100.0%; Pred. No. 0.0071; tive 0; Mismatches 0; Indels ; NUMBER OF SEQ ID NOS: 76 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 26 ; LENGTH: 244 ; TYPE: PRT ; ORGANISM: Artificial sequence ; FEATURE: ; OTHER INFORMATION: NO24D01 scFv US-10-981-692-26 156 SGSTSNIGNNYVS 168 1 SCSTSNIGNNYVS 13 13; Conservative ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-880-748-1926 Best Local Similarity US-09-880-748-1926 Query Match Matches g ઠે

Search completed: October 14, 2005, 17:00:43 Job time : 92.4219 secs

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157 SGSTSNIGNNYVS 169

1 SGSTSNIGNNYVS 13

(OTASU) NNAJB 39A9 SIHT

C007 77.66.07

OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 18.0781 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-13 66 1 SGSTSNIGNNYVS 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0	Description		g lambda	d lambda	a lambda	a lambda	d lambda chain	lambda	q lambda chain	g lambda chain	g lambda chain	q lambda	d lambda chain	q lambda chain	g lambda chain	a lambda chain	lambda 1	a lambda chain	a lambda chain	lambda	J lambda	J lambda	3 lambda	J lambda	Iq lambda chain pr	lambda chain	lambda	Jambda	1 ambda	
COLUMNICO	Ω	536050	847009	S19664	A29700	S25742	S05270	809712	LIHUBL	S47185	S24321	LIHUNW	S36048	LIHUNG	S78058	S78057	LIHUEP	836046	825757	C44151	A42193	S36047	S36258	D44151	823627	S25752	A44151	B44151	575	467
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	Score	62	62	62	62	62	62	20	57	26	26	22	23	53	23	23	52	20	49	48	4.	45					44	44	4	43.5
	Result No.	7	7	e	4	S	9	7	œ ·	9	01	11	12	13	14	15	16	17	18	19	20	12	7 6	523	57	25	56	27	28	53

abda abda	gag, pol and env p hypothetical prote	lambda lambda	uncharacterized co Ig lambda chain -	Ig lambda chain v Ig lambda chain v-	19 Identity - 5-aminola Chain V- 5-aminolavulinate Id lambda chain V-	lambda lambda
849571 S23626	T18572 G71609 S57428	S57408 S25744	F96997 S36054	B46516 L6HULT L1HTMM	A71646 L1HUWA	L1HUHA JE0246
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65	63 63 63	63.63	62	62.1	60	09
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30	337	36 36	38	339 410	42 43	4 4 5

ALIGNMENTS

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RESULT 1 836050 191 Jambda chain - human (fragment) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 R;Williams, S.C. submitted to the EMBL Data Library, April 1993 A;Reference number: 836046 A;Reference number: 836050 A;Retens: preliminary A;Molecule type: DNA A;Residues: 1-98 «MIL»	A, Cross-references: EMBL: Z22191; NID: 9312298; PIDN: CAA80201.1; PID: 9312299 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F: 15-91/Domain: immunoglobulin homology < IMM>	Gaps		
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1995	PIDN: globu	B 2; 001; 8		
-Dec-	298; nmuno n	Score 62; DB 2; Pred. No. 0.001; 1; Mismatches		
on 01 pril	9312; n; ir bulir gy <]	re 62 d. No Misma		
t) viBic ry, A	NID: regio noglo	Sco Pre 1;		
RESULT 1 536050 Cando chain - human (fragment) C;Species: Homo sapiens (man) C;Species: A2-Nov-1993 #sequence_revision 01-Dec-Cibate: 22-Nov-1993 #sequence_revision 01-Dec-R;Williams, S.C. Submitted to the EMBL Data Library, April 1993 A;Accession: 836046 A;Status: preliminary A;Melsidues: 1-98 eWIL>	A;Cross-references: EMBL:Z22191; NID:g312298; PIDN:CAA80201.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:15-91/Domain: immunoglobulin homology <imm></imm>	Query Match 93.9%; Score 62; DB 2; Length 98; Best Local Similarity 92.3%; Pred. No. 0.001; Matches 12; Conservative 1; Mismatches 0; Indels	13	32
(fri (mai gquen gata)	L: Z2; obul; mer; lobu]	92 vativ	1 SGSTSNIGNNYVS 13	zs sessanignnyvs 35
humar piene 3 #se 0 MBL D MBL D ary NA	: EMB unogl tetra	arity onger	GSTSNIGNNYV	N I GN
in - no sa 33605 33605 33605 11 min 10 min 10 min 10 min	imm imm itero	imil.	SGST:	2655
t cha: 1: Horizon: 2001: 3001: 4001: 5001: 5001: 5001: 5001: 5001: 5001: 5001: 5001: 5001: 5001:	efere mily: s: he omair	atch cal S	٦ ,	73
RESULT 1 836050 (19 lambda chain - human (frag) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence C;Accession: S36050 R;Williams, S.C. submitted to the EMBL Data Li A;Reference number: S36046 A;Reference number: S36046 A;Retus: preliminary A;Nolecule type: DNA A;Residues: 1-98 < WIL>	oss-r perfa yword -91/D	Query Match Best Local Similarity 92 Matches 12; Conservative		
RESULT 336050 Ig lam, C;Spec. C;Date C;Accel R;Will. 8ubmit A;Refe: A;Accel A;Accel A;Molec	A; Cr C; Suj C; Ke	A B B B	ठे व	2

RESULT 2
847009

Ig lambda chain VI-J3 region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: S47009
R;Mahmoudi, M.; Gaayna, E.; Denomne, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody binc
A;Reference number: S47009
A;Accession: S47009
A;Accession: S47009
A;Accession: S47009
A;Reatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <AMA+>
A;Cross-references: EMBL:Z35495; NID:G517346; PIDN:CAA84629.1; PID:G517347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-91/Domain: immunoglobulin homology <IMM>

Gaps ö Query Match 93.9%; Score 62; DB 2; Length 111; Best Local Similarity 92.3%; Pred. No. 0.0011; Matches 12; Conservative 1; Mismatches 0; Indels

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1 SGSTSNIGNNYVS 13

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Subvita

Ig lambda chain V region - human

Ig lambda chain V region - human

Ig lambda chain V region - human

C;Species: Homo sapiens (man)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 21-Jan-2000

C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 21-Jan-2000

C;Bupchem: J. 268, 135-140, 1990

A;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

B;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

A;Reference number: S09712

A;Reference number: S09712

A;Reference number: S09712

A;Residues: 1-130 cHUG>

A;Residues: 1-130 cHUG>

A;Residues: 1-130 cHUG>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Reywords: heterotetramer; immunoglobulin

F;34-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA

A Residues: 1-23 c KISI.)

A Residues: 1-23 c KISI.

A Cross-references: BMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

A Cross-references: BMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of A;Title: Nucleotide sequences of the CDNAs encoding the V-regions of H- and L-chains of A;Reference number: S04601; MUID:89296497; PMID:2500644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Aun.1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
CiAccession: S0270; S04601
Rikishimoto, T.
Submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Reference number: S05270
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Сарв
             A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Residues: 1-232 <COM>
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-130 «KIS2»
A;Cross-references: EMBL:X14583
A;Cross-references: EMBL:X14583
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted «SIG»
F;21-215/Poroduct: Ig lambda chain #status predicted «MAT»
F;150-218/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.0025;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Length 232,
                                                                                                                                                                                                                                                                                                                                                                    Query Match
93.9%; Score 62; DB 2; Length 232
Best Local Similarity 92.3%; Pred. No. 0.0025;
Matches 12; Conservative 1; Mismatches 0; Indels
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Local Similarity 92.3%;
hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 SGSSSNIGNNYVS 51
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A; Accession: S25742
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C;Species: Homo sapiens (man)
C;Species: Low-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 825742
R;Combriato, G: Klobeck, H.G.
Birr. J: Immunol. 21, 131-1522, 1991
A;Title: V(Lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Fitle: V(Lambda) and J(lambda)-C(lambda) PMID:1904362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Eulitz, M.; Breuer, M.; Linke, R.P.
Biol. Chem. Hoppe-Seyler 368, 863-870, 1987
A;Title: Is the formation of AL-type amyloid promoted by structural peculiarities of imm
A;Reference number: A29700; MUID:87299022; PMID:3620114
                                                                                                                                                                                                        ig lambda chain V region (clone alpha-phOx15) - human (grambda chain V region (clone alpha-phOx15) - human (species: Homo sapiens (man) (species: Homo sapiens (man) (species: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 (species: 22-Jan-1993 #sequence_revision 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 (species in the space in the species in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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C;Spacies: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Residues: 1-110,'W' <-JON>
A,Residues: 1-110,'W' <-JON>
A,Cross-references: EMBL:X61641; NID:g35458; PIDN:CAA43822.1; PID:g1335271
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Molecule type: protein
A;Residues: 1-113 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.0012;
....rrhes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1991
A;Reference number: $24442
A;Accession: $24444
A;Molecule type: mRNA
A;Residues: 1-110,'W' <JON>
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92.3%;
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Best Local Similarity 92.3%;
Matches 12; Conservative 3
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Best Local Similarity 92.3.
Best Local Similarity 92.3.
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                               SGSSSNIGNNYVS 35
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Gaps ö Score 59; DB 2; Length 130; Pred. No. 0.0045; 2; Mismatches 0; Indels Query Match

Best Local Similarity 84.6%;
Matches 11; Conservative 1 SGSTSNIGNNYVS 13

42 SGTSSNIGNNYVS 54

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Ig lambda chain precursor V-I region (BL2) - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacte: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Daccession: A01966
R;Tsujimoto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A;Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
A;Reference number: A01966; MUID:85062823; PMID:6095199

A,Molecule type: mRNA A,Residues: 1-130 <TSU> A,Cross-references: UNIPROT:P06316; GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087

C;Genetics:

A;Gene: GDB:IGLV@
A;Gene: GDB:IGLVG
A;Gene: GDB:IGLCG
A;Gene: GDB:

ö Length 130; 0; Indels DB 1; Score 57; DB 1; Pred. No. 0.01; 2; Mismatches 86.4%; Best Local Similarity 84.6 Matches 11; Conservative Query Match

1 SGSTSNIGNNYVS 13

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42 SGSSSNIGNDYVS 54

Ig lambda chain - human (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: O6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47185
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
R;McIntosh, Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien A;Reference number: S47181
A;Accession: S47185
A;Accession: S47185
A;Status: preliminary
A;Aolecule type: mRNA
A;Residues: 1-111 cMCI>

A;Cross-references: EMBL:X79782; NID:g506428; PIDN:CAA56178.1; PID:g506429 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;14-90/Domain: immunoglobulin homology <IMM>

ö Length 111; 1; Indels 84.8%; Score 56; DB 2; 84.6%; Pred. No. 0.013; ive 1; Mismatches Best Local Similarity 84.6 Matches 11; Conservative Query Match

1 SGSTSNIGNNYVS 13 |||:|||| |||| SGSSSNIGKNYVS 34

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C;Accession: \$24321
R;Aucouturier, P:; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne, Biochem. J. 285, 149-152, 1992
Biochem. J. 285, 149-152, 1992
A;Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pre A;Reference number: \$24319; MUID:92344562; PMID:1379039
A;Accession: \$243131
A;Acces S24321

Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Species: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24321
C;Accession: S24321
C;Accession: A: Rhamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchar.

Gaps ö Score 56; DB 2; Length 131; Pred. No. 0.015; 1; Mismatches 1; Indels 84.8%; 84.6%; Query Match
Best Local Similarity 84.6
Matches 11; Conservative

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8 셤 RESULT 11

Ignamoda chain V-I region (New) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01964
R;Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A;Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subgr
A;Reference number: A01964; MUID:69060892; PMID:4177823

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Gaps

A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein.
A;Conser-feferences: UNIPROT:P01701
C;Comment: This is a Bence Jones protein.
C;Comment: This is a Bence Jones protein.
C;Complex: A;Gene: GDB:IGLV@
A;Cross-references: GDB:I19342; OMIM:147240
A;Crosplex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp A;Crosplex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp C;Cropplex: Diocked maino end; heterotetramer
C;Complex: blocked maino end; heterotetramer
C;Superfamily: immunoglobulin homology
C;Superfamily: immunoglobulin homology
F;15-91/Domain: immunoglobulin homology
F;15-91/Domain: immunoglobulin homology
F;15-91/Domain: immunoglobulin homology
F;12-91/Domain: immunoglobulin homology
F;12-91/Domain: immunoglobulin homology

Gape ö 83.3%; Score 55; DB 1; Length 111; 76.9%; Pred. No. 0.019; 1ve 2; Mismatches 1; Indels Query Match Best Local Similarity 76.9 Matches 10; Conservative

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RESULT 12

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Gaps

Si6048
Ig lambda chain - human (fragment)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiAccession: Si6048; Si6049
R;Williams, S.C.

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Search completed: October 14, 2005, 16:23:38 Job time : 18.0781 secs
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A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22411.-2-22411.6
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;IS-91/Domain: immunoglobulin homology <IMM'
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu F;22-89/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-129 < HAR>
A; Residues: 1-129 < HAR>
A; Cross-references: EMBL:XS4446; NID:g37923; PIDN:CAA38313.1; PID:g930121
A; Cross-references: EMBL:XS4446; NID:g37923; PIDN:CAA38313.1; PID:g930121
B; Harattero, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 33-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
Cispace: 03.Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
Cispacesion: A01965
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
A;Title: Comparative studies on the structure of the light chains of human immunoglobuli A;Reference number: A91970; MUID:81186114; PMID:6404900
                                                                                   A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Residues: 1-98 <WIL>
A;Residues: 1-98 <WIL>
Cross=references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 111;
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                                                                                                                                                                                                                                                                                                                                                    Length 98
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A,Reference number: S23716; MUID:92031262; PMID:1718404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.3%; Score 53; DB 1;
76.9%; Pred. No. 0.042;
rative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 2;
Pred. No. 0.037;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, August 1990 A;Reference number: S78051 A;Accession: S78058
to the EMBL Data Library, April 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Cross-references: UNIPROT:P01702
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                              Reference number: S36046; Accession: S36048
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Best Local Similarity
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A;MOlecule type: mRNA
A;Residues: 1-130 <HAR>.
A;Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
A;Cross-references: EMBL:X54438; NID:g37920; H.; Burastero, S.E.; Wilder, R.L.; Notkins,
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins,
Int. Immunol. 3, 865-875, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Int. Immunol. 3, 865-875, 1991 A; the genes encoding the V(H) and V(L) regions of low- and hi A; Title: Complete sequence of the genes encoding the V(H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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A; Accession: S23723
A; Molecule type: mRNA
A; Residues: 19-129 «HAM»
A; Residues: 19-129 «HAM»
A; Cross-references: EMBL:X54446
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 1-18/ Domain: signal sequence (fragment) #status predicted «SIG»
F; 19-129/ Product: Ig lambda chain (fragment) #status predicted «MAT»
F; 33-109/ Domain: immunoglobulin homology «IMM»
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83.3%; Pred. No. 0.049;
1ive 2; Mismatches 0; Indels
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Pred. No. 0.049;
2; Mismatches
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Best Local Similarity 83.3%;
Matches 10; Conservative ;
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A, Residues: 20-130 <HAW>
A, Cross-references: EMBL:X54438
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US-10-614-959-13 66 1 SGSTSNIGNNYVS 13 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

1612378 seqs, 512079187 residues

Searched:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		op.				
Result	or CO	Query	Query Match Length	2	£	
		110000	TI STORY	9 !	14	Description
н	57	86.4	130	н	LV1G HUMAN	P06316 homo sapien
7	26	84.8	101	N	Q8IZD8	рошоц
e	55	83.3	110	~	QSTE63	рошо
4	. 22	83.3	111	Н	LV1C HUMAN	homo
ស	53	80.3	108	~	Q96S <u>B</u> 0	homo
ø	23	80.3	111	Н	LV1D HUMAN	homo
7	25	78.8	109		LV11 HUMAN	homo
80	52	78.8	235	~	061N <u>9</u> 9	homo
O	51	77.3	236	~	Q8NEJ1	homod
10	49	74.2	237	~	Q6DHW4	homo
11	45	68.2	235	~	QGGMWG	homo
12	44			N	087LH3	
13	44	66.7		~	Q78CJ5	
14	44	66.7		7	Q8JRX2	
15	43	65.2	1170	~	6NZMLO	
16	43	65.2	1357	7	Q9W4M4	•
17	43	65.2	2186	٦	YL52 CAEEL	-
18	43		2272	7	017329	Q17329 caenorhabdi
19	43		2500	~	096223	
20	42	63.6	236	N	Q6GMV7	
21	42	63.6	348	~	Q97KX3	clost
22	42	63.6	633	-	ACES ELEEL	
23	41	62.1	111	-	LV6D_HUMAN	P06318 homo sapien
24	41	62.1	112	-	LV1H HUMAN	P06887 homo sapien
22	41	62.1	388	~	Q9VRW7	Q9vrw7 drosophila
56	41	62.1	414	-	HEM1_RICPR	Q9zcb8 rickettsia
27	41	62.1	414	~	Q68VS3	Q68vs3 rickettsia
28	41	62.1	847	~	Q6BK59	_
59	41	62.1	958	~	Q7RRT8	
30	41	62.1	1272	~	Q95SG4	
31	41	62.1	1272	7	Q9W117	Q9w117 drosophila

e2 drosophila a0 drosophila 50 plasmodium 108 homo sapien 100 homo sapien 11 caenorhabdu 11 caenorhabdi 12 secherichia 13 francisella 15 neurospora 167 anopheles g 147 mycoplasma
0811e2 081180 081150 081150 P04208 P01700 08418 08418 095162 077259 077254
QBIJE2 QBIJA0 QBIJS0 LVIF_HUMAN LVIB_HUMAN QBGFB2 QPFE2 QPFE2 QPFE2 QPFE2 QP7F25 QP7F29 QP7F29 QP7F29 QP7F29 QP7F29 QP7F29
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1298 1336 1701 100 1109 1109 1109 1109 1109 1109
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ALIGNMENTS

1 SGSTSNIGNNYVS 13

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Gaps

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Query Match
86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.069;
Matches 11; Conservative 2; Mismatches 0; Indels

QBIZD8

RESULT 2 Q81ZD8

1 SGSTSNIGNNYVS 13

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Langer B., Steinmetz-Kayne M., Hilschmann N.; "The complete amino acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98375893; PubMed-9712075; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson B.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis; human anti-N-acety1glucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 55; DB 1; Length 111; 76.9%; Pred. No. 0.13; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   type). Subgroups in the variable part of immunoglobulin L. the lambda-type.";
the lambda-type.";
Hope-Seyler's Z. Physiol. Chem. 349:945-951(1968).
-!- MISCELLANDUS: This is a Bence-Jones protein.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A01964; LiHUNW.
HSSP; PO1703; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrrolidone carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 111
111 Aa; 11453 MW; AAECBCA3C49F2AD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region NEW.
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                                                                                                                111 AA.
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                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                  MEDLINE=69060892; PubMed=4177823;
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Homo sapiens (Human).
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              23 SGTSSNIGNNFVS 35
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                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                 HUMAN
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DISÜLFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE—95007525; PubMed=7923137;
Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
"Egtablishment, molecular rescue, and expression of 123AV16-1, a tumor-reactive human monoclonal antibody.";
cancer Res. 54:5778-5185(1994).
EMBL; L33985, AAL68704.1;
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin light chain variable
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84.6%; Pred. No. 0.079;
tive 1; Mismatches 1; Indels
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                                                                                                                   0; Indels
                                                                                                                                                                                                                                                        110 AA; 11479 MW; 599D1628F8F5437C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-Mmunglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 AA
                                                                                     101 AA.
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                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                  EMBL: AY146444; AAN64328.1; -..
HSSP; P01703; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SGSTSNIGNNYVS 13
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Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 84.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                     PRELIMINARY;
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   42 SGSSSNIGNDYVS
                                                                                                                                                                                       Homo sapiens (Human)
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Query Match

Matches

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RESULT 3

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Gaps

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NON TER SEQUENCE Query Match

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MEDLINE=86000126; PubMed=3929803;
Toft K.G., Sletten K., Husby G.;
"The amino-acid sequence of the variable region of a carbohydrate-
containing amyloid fibril protein BPS (immunoglobulin light chain,
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 104 N-linked (GlcNAC. .).
22 89 By similarity.
109 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
                                01-JAN-1988 (Rel. 06, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 1 lambda chain V-I region EPS. Homo sapiens (Human).
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NON TER
SEQUENCE
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Q61N99
                                   DTT BE SEED TO BE SEED
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDINE-81186114; PubMed=6404900;
MEDINE-81186114; PubMed=6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T., Shimizu A.;
                                                                                                                                                                                                                                                                                                            80.3%; Score 53; DB 2; Length 108;
83.3%; Pred. No. 0.28;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.3%; Score 53; DB 1; Length 111; 76.9%; Pred. No. 0.29; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig-like.
Pyrrolidone carboxylic acid.
By similarity.
                                                                                                                                                                                                                                  NON TER 1 1 1 SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 89 By similarity.
111 111
111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1. PROSITE; PS50815; IG LIKE; 1. Direct protein sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig lambda chain V-I region NIG-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA
             antibody V region genes.";
J. Immunol. 16:2020-2031(1998).
EMBL; 196394, AAB68783.1;
PDB; 1KU4; MOG41, L=1.008.
INEAFPC; IPRO07310; Ig-like.
InterPro; IPRO03596; Ig-V.
SMART; SMO0406; IGV: I.
PROSITE; PSS0035; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Best Local Similarity 76.9'
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.3
Matches 10; Conservative
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P01702;
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LV1D HUMAN
AC P01702.
DT 21-JUL.
DT 21-JUL.
DT 21-JUL.
DT 21-JUL.
DT 21-JUL.
DE 19 land
DE 19 land
DE 20. Human];
OC Mammal;
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OC Mammal;
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OC Mammal;
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OC MAMMAN;
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Ig-like. N-linked (GlcNAc. ..). By Bimilarity.

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubsberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
Straubsberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Brows S.S., Loquellano N.A., Peters G.J., Abramaon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                           Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                               78.8%; Score 52; DB 1; Length 109; 83.3%; Pred. No. 0.42; tive 1; Mismatches 1; Indele
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Q6IN99;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGLC2 protein.
Name=IGLC2;
                                                                                                    Conservative
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Query Match
Best Local Similarity
----- 10; Conserv?
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109 AA.

LV1I HUMAN STANDARD; P06888; 01-JAN-1988 (Rel. 06, Created)

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CDNA
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Ra Stransberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ra Altend S.E., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Rableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzny D.M., Soderger B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rabakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
T. Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeelby R.W., Touchman J.W., Green E.D., Dickson M.C., Krimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                              InterPro; IPR001359; Ig.
InterPro; IPR001310; Ig-like.
InterPro; IPR0033006; Ig-like.
InterPro; IPR0033006; Ig-like.
InterPro; IPR003596; Ig-u.
Pfam; PP07654; Cl-set; I.
SWART; SW00407; IG.2.
SWART; SW00407; IG.1; I.
SWART; SW00406; IGV; I.
PROSITE; PSS0835; IG_LIKE; 2.
PROSITE; PSS0835; IG_LIKE; 2.
PROSITE; PSS0835; IG_LIKE; 2.
PROSITE; PSS0835; IG_MHC; UNKNOWN I.
SEQUENCE 235 AA; Z4888 MW; 90C95D5E87A6BCCI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072392; AAH72392.1; -.
HSSP; P01042; 1AQK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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nes 10; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                              SEQUENCE FROM N.A. TISSUE-Pancreas;
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EXCURDACE FROM N.A.

TISSUE=Primary B-Cells;

RA NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA NEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L. Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.E., Zeeberg B., Bueccow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.E., Zeeberg B., Bueccow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.E., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheefer T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA S.A., Loquellano N.A., Pecers G.J., Abrameon R.D., Mullahy S.J.,

Rachas S.A., McEwan P.J., McKertan K.J., Malek J.A., Guneratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley W.G., Sodergren B.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radirguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radirguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radirguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radirguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield W.B.,

Razywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

Radenration and initial analysis of more than 15,000 full-length human means and mones an
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC030984; AAH30984.1; -.
HSSP; P01703; 7FAB.
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SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
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InterPro; IPR007110; IG-like.
InterPro; IPR003597; Ig.cl.
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Homo sapiens (Human).
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X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Febingold E.A., Grouse L.H., Derge J.G.,

A Alausberg R.L., Febingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buedow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Robinstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human R.P.

"Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
IPEan; PP007554; C1 set; I.
Pfam; PP0047; Ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches 10; Conservative
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OGGMWA
AC OGGMW
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STRAIN=RIMD 2210633 / Serotype O3:K6;
STRAIN=RIMD 2210633 / Serotype O3:K6;
STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; Pubmed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakamo M., Yamashita A., Kubota Y.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
EMBL, AP05092; BAC60902.1;
                                                                                                                                                       Gaps
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STRAIN=OR74A;
Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
1711_TaxID=670;
                                                                                                         68.2%; Score 45; DB 2; Length 235; 69.2%; Pred. No. 14; tive 3; Mismatches 1; Indela
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Pred. No. 20;
2; Mismatches 2; Indels
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 235 AA; 24803 MW; 058B05F61118F1B8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annotation update)
Putative short-chain dehydrogenase.
OrderedLocusNames=VP2639;
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Last sequence update)
Last annotation update)
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR02198; ADH-short.
InterPro; IPR031347; Adh-short_C2.
                                                                                                                                                                                                                                                                                                                                              221 AA
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01-MAR-2004 (TrEMBLrel. 26, C;
01-MAR-2004 (TrEMBLrel. 26, L;
01-MAR-2004 (TrEMBLrel. 26, L;
Hypothetical protein.
Name=NCU00836.1;
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PRINTS; PR00081; GDHRDH.
                                                                                                  Query Match
Best Local Similarity 69.2<sup>3</sup>
Matches 9, Conservative
                                                                                                                                                                                        1 SGSTSNIGNNYVS 13
                                                                                                                                                                                                                   42 SGSSSNIGSNSVN 54
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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1es 8; Conservative
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SEQUENCE 221 AA;
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Q87LH3
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Q7SCJ5
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(TremBirel. 25, Created) (TremBirel. 25, Last sequence update) (TremBirel. 26, Last annotation update)

PRT; 1170 AA

PRELIMINARY;

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STRAIN=PA14;
PubMed=14983043; DOI=10.1073/pnas.0304622101;
PubMed=14983043; DOI=10.1073/pnas.0304622101;
He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
Lee D., Urbach J., Goodman H.M., Rahme L.G.;
"The broad host range pathogen Pseudomonas aeruginosa strain PA14
carries two pathogenicity islands harboring plant and animal virulence
                                                                                                                                      Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535 (2004). EMBL, AY273871, AAP81276.1; -. Interpro, IPR008707, Neisseria PilC. Pfam, PF05567; Neisseria PilC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70...
7, Conservative
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=287;
                                           01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
PilY1.
                                                                                                                     Name=pilY1;
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                                                                                                                                                                                                                                                                                                                                                                           genes."
       Q7WZN9
         ð
                                                                                                                                                                                                                                                                                           C.-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, ABEXO1000101; EAA34466.1; -..

EMBL, ABEXO1000101; EAA34466.1; -..

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005577; P:carbohydrate metabolism; IEA.

InterPro; IPR005103; Glyco_hydro_61.

PROM: PF00734; CBM_1; 1.

PROSITE; PS00562; CBD_FUNGAL: 1.

PROSITE; PS00562; CBD_FUNGAL: 1.

ROSITE; PS00562; CBD_FUNGAL: 1.

ROSITE; PS00562; CBD_FUNGAL: 1.
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schlitcenlikoff C.P., Kinney J.A., Braun E.L., Zelter A., Schulte U., A. Kothe G.O., Jedd G., Mawes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., A., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rammusen C., Macrenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Fratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbacch M.J., Berglund J., Voelker R., Aramayo R., Martyg D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freiteg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 44; DB 2; Length 326; 61.5%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 61.5%;
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Search completed: October 14, 2005, 16:19:55 Job time: 88.5312 secs
139 GSTTNLSNNY 148
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Gaps

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3; Indels

2; Mismatches

311 SGSTCKVGNDYYS 323

1 SGSTSNIGNNYVS 13

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2; Indels

2; Mismatches

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Best Local Similarity 66...
8; Conservative

264 SGNLFNIGNNYL 275

RESULT 15

O7WZN9

1 SGSTSNIGNNYV 12

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66.7%; Score 44; DB 2; Length 441; 66.7%; Pred. No. 41;

Pfam; PF05098; LEF-4; 1. SEQUENCE 441 AA; 51639 MW; DC7B3982232E3550 CRC64;

Phthorimaea operculella granulovirus. Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus. NCBI_TaxID=192884;

01-OCT-2002 (TrEMBLrel. 22, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-UN-2003 (TrEMBLrel. 24, Last annotation update) Late expression factor 4.

441 AA

PRT;

PRELIMINARY;

QBJRX2; Q8JRX2

RESULT 14

SECUENCE FROM N.A. Croizier G., Lopez Ferber M.; Croizier E., Taha A., Croizier G., Lopez Ferber M.; Submitted (ERP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF499596; AAM70285.1; -. GO:0030528; F:transcription regulator activity; IEA. GO; GO:0045449; P:regulation of transcription; IEA. InterPro; IPR007790; LEF-4.

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Gaps

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65.2%; Score 43; DB 2; Length 1170; 70.0%; Pred. No. 1.6e+02; Live 2; Mismatches 1; Indels

1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;

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October 14, 2005, 15:51:19 ; Search time 53.8125 Seconds (without alignments) 50.310 Million cell updates/sec е :: Run

US-10-614-959-14 Perfect score:

1 DVSKRPS 7 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003ss:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ady79072 Anti-fact Adj80338 Vlambda g Aau02544 Anti-adip Aau02558 Anti-adip Aau02612 Anti-adip Aau02612 Anti-adip Aau02629 Anti-adip Aau02629 Anti-adip Aau02629 Anti-adip Aau02639 Anti-adip Aau02551 Anti-adip Aau02551 Anti-adip Adu02561 Anti-adip Adu0268 Anti-adip Adu02694 Anti-adip Ady17416 Anti-adip Ady17416 Anti-huma Ady1888 Human Biy Ady1889 Human Biy Ady188714 Single ch Ady66714 Single ch Ady46044 Human Biy Ady366714 Single ch Ady366718 Single ch Ady36718 Single ch	
SUMMARIES	AAY79072 ADU80338 AAU02544 AAU02544 AAU02548 AAU02612 AAW19883 AAW12542 AAW12542 AAW12542 AAW12542 AAW12542 AAW12542 AAW12542 AAW12542 AAW12542 AAW12551 AAW12515 AAW12515 AAW12515 AAW12515	
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ALIGNMENTS

AAY79072 standard; peptide; 7 AA. RESULT 1 AAY79072

AAY79072;

(first entry) 12-JUN-2000 Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence

Complementarity determining region 2; CDR2; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venoue thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome, ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC.

ä Kirchhofer Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction. CCCCCX88X44X8X111X48X3X6X8X8X8X8X84X411X68X6X6CCCCX88X6

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine processe that participates in the blood coaqulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/TXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary artery bypass graft (LABG), percutaneous transluminal coronary angloplastry (PTCA), stroke, tumour growth, invasion or metaersais, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
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Sequence 7 AA;

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; Score 35; DB 3; Length 7; Pred. No. 1.8e+06; 0; Mismatches 0; Indels
          100.0%;
Query Match
Best Local Similarity luv.
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Gaps ö

> ADJ80338 standard; protein; 99 AA. DVSKRPS 7 ADJ80338; RESULT 2 ADJ80338

hybrid antibody; antibody; framework region; homology; immunogenicity. Vlambda gene locus antibody amino acid sequence #7. 03-DEC-2002; 2002WO-US038450 03-DEC-2001; 2001US-0336591P 06-MAY-2004 (first entry) 402003048321-A2 Ношо варіепв 12-JUN-2003

Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.

(ALEX-) ALEXION PHARM INC

Wu D;

Rother R,

WPI; 2003-513753/48.

Disclosure; SEQ ID NO 98; 77pp; English.

The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (1) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable cregion of the initial antibody; (iii) selecting a first component of the catabase of antibody sequences contained in a reference sequence of the first component to sequences contained in a reference catabase of antibody sequences or antibody fragment sequences from a target species; (v) selecting a sequence from an antibody in the database which demonstrates a high degree of homology to the first component; (vi) selecting a second component of the variable region which is different the first component, the second component selected from the group consisting of FRI, FR2, FR3 and FR4; (vii) comparing the sequence of the second component to sequences contained in a reference database of the antibody sequences or antibody fragment sequences from the target species (viii) selecting a sequence from the database which demonstrates a high degree of homology to the second component and which is from a different antibody than the selected antibody; and (ix) operatively linking the

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
condition. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
ceternalment be presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies

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selected framework sequences to one or more complementarity determining regions (CDRs) of the initial antibody to produce a hybrid antibody or hybrid antibody fragment. The method is useful for producing a hybrid antibody or hybrid antibody fragment (claimed). The antibody and fragments are useful for therapeutic and diagnostic purposes. The method uses entire framework regions from a single antibody variable heavy or variable light chain to receive the CDRs. This produces antibodies that are highly homologous and exhibit reduced immunogenicity while maintaining an optimum binding profile. This sequence represents the amino acid sequence of an antibody from the Vlambda gene locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        fat;
                                                                                                                                                                                  100.0%; Score 35; DB 7; Length 99; 100.0%; Pred. No. 5.4; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-adipocyte monoclonal antibody light chain, FAT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                              AAU02544 standard; protein; 109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 120; 182pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                 Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                             Sequence 99 AA;
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for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                     100.0%; Score 35; DB 4; Length 109; 100.0%; Pred. No. 6; Store 0; Mismatches 0; Indels
                                                                                                                                              Local Similarity 100.
                                                                        Sequence 109 AA;
                                                                                                                        Query Match
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51 DVSKRPS 57 1 DVSKRPS 7 ò 셤

RESULT 4

AAY96060 standard; protein; 110 AA.

05-DEC-2000 (first entry)

Human anti-DAF antibody LU30 light chain variable region.

LU30; human; antibody; VL domain; decay accelerating factor; DAF phage display; subtractive panning; lung cancer; lung carcinoma; lung adenocarcinoma; therapy; diagnosis.

Homo sapiens

91...100 /label= CDRIII /note= "complementarity determining region III" 93...99 /note= "hypervariable loop residues" 52. 58 /label= CDRII /note= "complementarity determining region II" "complementarity determining region I" .54 ce= "hypervariable loop residues" .35 :e= "hypervariable loop region" Location/Qualifiers 23. .36 /label= CDRI 'note= note= Key Region Region Region Region Region Region

40200052054-A2

08-SEP-2000

29-FEB-2000; 2000WO-US005352

(GETH) GENENTECH INC

99US-0122262P

01-MAR-1999;

Carter PJ, Ridgway JB; WPI; 2000-594169/56.

Making antibodies (e.g. anti-decay accelerating factor antibody) for diagnosing or treating e.g. lung cancer comprises identifying an antigen that is differentially expressed on the surface of two or more distinct cell populations. Making

Disclosure; Fig 5A; 52pp; English.

The present sequence is that of the light chain variable region (VL) of the anti-decay accelerating factor (DAF) human antibody LU30. The VH region is given in AAY06063. LU30 has a binding affinity (Kd) for DAF of about 13 nM. It was produced using a novel method for making antibodies which can be used for cancer diagnosis or therapy. The method comprises:

live cancer cell; (b) selecting an antibody phage library to a live cancer cell; (b) selecting an antibody phage or antibody which binds selectively to the live cancer cell; and (c) identifying an antigen to which the antibody phage or antibody binds. To obtain LU30, a human acry library was used to search for tumour-associated antigens by panning the cumour bronchial epithelial cell line, BEAS-2B. The invention also describes a method for identifying an antigen which is differentially expressed on the surface of 2 or more distinct cell populations. The antice of the composition comprising the antibody, or a composition comprising the antibody, is useful for in vivo cancer diagnosis or therapy. In particular, the antibody is useful for diagnosing or treating lung cancer, e.g. small-cell lung cancer, non-small cell lung cancer, large cell lung carcinoma, lung 8X88888888888888X8

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Sequence 110 AA;

Gaps ö 100.0%; Score 35; DB 3; Length 110; 100.0%; Pred. No. 6.1; or Mismatches 0; Indels 0; Indela Query Match Best Local Similarity 100.vv Best Local 7; Conservative 1 DVSKRPS 7 ઠે

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DVSKRPS 58

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AAU02558 Btandard; protein; 110 AA. RESULT 5 AAU02558

(first entry) 29-AUG-2001 AAU02558;

Anti-adipocyte monoclonal antibody light chain, FAT 44

fat; Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.

Homo sapiens.

WO200127279-A1.

11-OCT-2000; 2000WO-GB003900.

99US-0158812P 12-OCT-1999; (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Edwards BM, Main SH, WPI; 2001-282031/29. N-PSDB; AAS03458. Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 128-129; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obselty and obserty related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the

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Matches

Query Match Best Local Similarity

DVSKRPS 57

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DVSKRPS 7

100.0%; Score 35; DB 4; Length 110; 100.0%; Pred. No. 6.1;

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presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
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                                                                                                                                                                                                                                                                                                                                     Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                             AAU02612 standard; protein; 110 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 163; 182pp; English
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N-PSDB; AAS03512.
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                                                                                      Sequence 110 AA;
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AAU02612
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

99US-0158812P

12-OCT-1999;

11-OCT-2000; 2000WO-GB003900.

W0200127279-A1. Homo sapiens.

19-APR-2001.

Edwards BM, Main SH, Vaughan TJ;

WPI; 2001-282031/29

N-PSDB; AAS03527

Anti-adipocyte monoclonal antibody light chain, FAT 112.

29-AUG-2001 (first entry)

AAU02627;

AAU02627 standard; protein; 110 AA.

RESULT 7 AAU02627

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid

condenses of anti-adipocyte monoclonal antibody heavy chain, light chain,

condenses of anti-adipocyte monoclonal antibody heavy chain,

condenses, the antibodies can be used in the treatment of obesity and

condenses. The antibodies can be used to deliver drugs or

condenses. The antibodies can be used to deliver drugs or

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condenses. The antibodies can be used to activate the immune system to destroy the cells

condense can be used to activate the immune system to destroy the cells

condense the methodies may be labeled with a

condense to a radiolabel, fluorescent or chemical group and

detectable label antiganosis in human subjects e.g. to determine the

condense of adipocyte antiganosis in human subjects in a cell or tissue sample.

condense can be used as an alternative means of treatment for obese

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1, Page 172; 182pp; English.
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ses 7; Conservative
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
or an be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods of diagnosis in human subjects e.g. to determine the
cused in methods of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposite can also be produced e.g. intraabdominal fat associated with heart disease

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2007 77:65:0T c
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Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                     Anti-adipocyte monoclonal antibody light chain, FAT 113.
                                                                                                                                                          (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
            .AAU02629 standard; protein; 110 AA.
                                                                                                                                                                       Edwards BM, Main SH, Vaughan TJ;
                                                                                                                                                                                                                                     Claim 1; Page 173; 182pp; English.
                                                                                                                              11-OCT-2000; 2000WO-GB003900
                                                                                                                                            12-OCT-1999; 99US-0158812P
                                      29-AUG-2001 (first entry)
                                                                                                                                                                                    WPI; 2001-282031/29.
N-PSDB; AAS03529.
                                                                                                    WO200127279-A1
                                                                                       Homo sapiens
                                                                                                                 19-APR-2001
                          AAU02629;
                                                                                                                                                                                                                       diseases
     RESULT 8
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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
con be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
complement mediated lysis in human subjects e.g. to determine the
consence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposite can also be produced e.g. intraabdominal fat associated with heart disease

Sequence 110 AA;

Gaps .; 0 100.0%; Score 35; DB 4; Length 110; 100.0%; Pred. No. 6.1; ive 0; Mismatches 0; Indels 0; Indels Query Match Best Local Similarity 100... 7; Conservative

||||||||| DVSKRPS 57 1 DVSKRPS 7

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AAW19883 standard; protein; 111 AA.

AAW19883; RESULT 9
AAW19883
ID AAW1
XX
AC AAW1
XX

CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.

Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.

Homo sapiens

Location/Qualifiers Region

23. .35 /label= CDR1 /note= "complementarity determining region 1"

Region

Region

90. .100 //label= CDR3 /note= "complementarity determining region 3" 50. 56 /label= CDR2 /note= "complementarity determining region

WO9720932-A1

12-JUN-1997

96WO-GB003043 09-DEC-1996; 95GB-00025004 07-DEC-1995;

96GB-00010824. 11-OCT-1996;

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY

Osbourn JK, Allen DJ, Mccafferty JG;

WPI; 1997-319779/29. N-PSDB; AAT72133. Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer.

Claim 14; Fig 1b; 128pp; English.

This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2 and CEA3. WH (AAA721213-15) and VL (AAA721313-15) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see AAM19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include yairings of VH and VL sequences from CEA1-7, or their CDR sequences, as well as CEA6 VH and VL variants. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for disgnosing cancer, e.g. adenocarcinoma of the colon, lung or breast

Sequence 111 AA;

Gaps ö Query Match 100.0%; Score 35; DB 2; Length 111; Best Local Similarity 100.0%; Pred. No. 6.1; Matches 7; Conservative 0; Mismatches 0; Indels

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RESULT 10 AAU02542 ID AAU0 XX AC AAU0

AAU02542 standard; protein; 111 AA.

AAU02542;

WO200127279-A1. Homo sapiens.

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
chesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
chectable label such as radiolabel, fluorescent or chemical group and
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                    Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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                                               Anti-adipocyte monoclonal antibody light chain, FAT 30.
                                                                                                                                                                                                                                                                                                                            (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 118-119; 182pp; English
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                                                                                                                                                                                                                                                                                                                                                                   Vaughan TJ;
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                                                                                                                                                                                                                                                      11-OCT-2000; 2000WO-GB003900
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                 29-AUG-2001 (first entry)
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid

sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,

and heavy chain complementarity determining regions (CDR) of the

invention. The antibodies can be used in the treatment of obesity and

cobesity related diseases. The antibodies can be used to deliver drugs or

cobesity related diseases. The antibodies binding specifically to

can be used as a therapeutic itself. Antibodies binding specifically to

adipocytes can be used to activate the immune system to destroy the cells

complement mediated lysis. The antibodies may be labeled with a

cy complement mediated lysis. The antibodies may be labeled with a

cy used in methods of diagnosis in human subjects e.g. to determine the

cy treather label antigen on the surface of an adipocyte to detect or

cy the antibodies can be used as an alternative means of treatment for obese

cy the antibodies can be used as an alternative means of treatment for obese

cy patients other than undergoing surgery to remove excess fat. Antibodies

cy different types of fat deposits can also be produced e.g. intra-

abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                    Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
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                                                                                                                                                                   CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02585 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 124; 182pp; English.
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                                                                                                11-OCT-2000; 2000WO-GB003900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                         dwards BM, Main SH,
                                                                                                                                                                                                                                          WPI; 2001-282031/29.
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                                                                                                                                      12-OCT-1999;
                                                                 19-APR-2001
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY BM, Main SH, Vaughan TJ;

99US-0158812P.

12-OCT-1999;

WPI; 2001-282031/29 N-PSDB; AAS03485.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.

Claim 1; Page 146; 182pp; English.

AAU02501-AAU02535, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
cobesity related diseases. The antibodies and be used to deliver drugs or
con be used as a therapeutic [test]. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
concepted can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
concepted in methods of diagnosis in human subjects e.g. to determine the
consence of adipocyte antigen on the surface of an adipocyte to detect or
concepted the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
concepted that undergoing surgery to remove excess fat. Antibodies
concepted the presence of fat deposits can also be produced e.g. intraconcepted the presence of the deposits can also be produced e.g. intraconcepted the presence of the presence of the deposits can also be produced e.g. intraconcepted the presence of the presence of the deposits can also be produced e.g. intraconcepted the presence of the presence of the presence of the deposits can also be produced e.g. intraconcepted the presence of the presence of the presence of the deposits can also be produced e.g. intraconcepted the presence of the deposits can also be produced e.g. intraconcepted the presence of the presence

Sequence 111 AA;

Query Match 100.0%; Score 35; DB 4; Length 111; Best Local Similarity 100.0%; Pred. No. 6.1; Matches 7; Conservative 0; Mismatches 0; Indels 1 DVSKRPS 7 ò

57 DVSKRPS 51

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ADK17416 standard; protein; 111 AA. ADK17416;

06-MAY-2004 (first entry)

Anti-human CXCR4 loop 6 ScFv antibody Vl region.

cytostatic; virucide; single chain antibody; antibody; yeast; HIV; cancer; anti-HIV;

Synthetic.

WO2003066830-A2.

14-AUG-2003

07-FEB-2003; 2003WO-US003763

08-FEB-2002; 2002US-00071866. 08-FEB-2002; 2002US-00072031. 25-APR-2002; 2002US-00133978.

(GENE-) GENETASTIX CORP

Pauling MH, Zhu L; Hua S,

WPI; 2003-731501/69.

Selecting an scFv against a peptide target by expressing a target fusion protein having a DNA binding domain or activation domain of a transcription activator, useful for diagnosing, preventing and/or treating HIV infection and cancer.

Claim 123; SEQ ID NO 61; 150pp; English

The invention relates to a method of selecting a single chain antibody (scFv) against a peptide target in a yeast by expressing a library of scr fataion proteins in yeast cells, expressing a target fusion protein can the yeast cells expressing the scFv fusion proteins having either the cartivator which send comprised in the scFv fusion proteins, and a cativator which is not comprised in the scFv fusion proteins, and a cativator which is not comprised in the scFv fusion proteins, and a cativator which school comprises either an activation of a sexpressed. Each scFv fusion protein comprises either an activation comparise of an activation of a sexpressed. Each scFv fusion protein comprises either an activation of a sexpression of a variable region (WH) of antibody whose sequence varies within the library, a light chain of a variable region (WL) of antibody whose sequence varies within the library independently of the captide which links the VH and VL. The expression of the cropsorter gene is activated by a reconstituted transcriptional activator formed by binding of the scFv fusion protein to the target fusion compositions of the present invention are useful for preventing and/or treating HIV infection and cancer. This sequence corresponds to the VI region of an anti-human CXCR4 loop 6 antibody gene and used to generate the scFv antibody of the invention.

Sequence 111 AA;

Gape ö 100.0%; Score 35; DB 7; Length 111; 100.0%; Pred. No. 6.1; ive 0; Mismatches 0; Indels 0; Indels Query Match
Best Local Similarity 100.
Matches 7; Conservative

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Gaps ö RESULT 14 ADG42838

ADG42838 standard; protein; 111 AA. ADG42838;

26-FEB-2004 (first entry)

scFv Ab124 light chain variable region.

HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver; renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon; lymphoma; leukaemia; pancreas; chemokine receptor; antibody.

Synthetic.

JS2003206909-A1.

36-NOV-2003.

08-FEB-2002; 2002US-00071866. 08-FEB-2002; 2002US-00072301. 25-APR-2002; 2002US-00133978. 07-FEB-2003; 2003US-00360828

(HUAS/) HUA S. (PAUL/) PAULING M H. (ZHUL/) ZHU L.

Zhu L; Pauling MH, fua S,

WPI; 2004-051479/05

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The invention relates to an antibody that binds to loop 6 of human chemokine receptor (CXCR4). The antibody is useful in the treatment or prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer of (e.g. breast, prostete, liver, renal, lung, skin, ovarian, cervical, brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer cells), for screening drugs, for diagnosing disease or condition associated with interaction with chemokine receptor. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SK, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                              Antibody binding loop of human chemokine receptor useful for the treatment of HIV infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human diagnostic and therapeutic pprotein SEQ ID NO:5321.
                                                                                     Claim 6; SEQ ID NO 61; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM85072 standard; protein; 214 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2003; 2003WO-US028227.
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Stevens KA, b...
-alta CH, Andersc...
Spiro PA, F
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Best Local Similarity
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Patury S, Shi X,
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N-PSDB; ADG42836
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                                                                                                                                                                                                                                                                                  Sequence 111 AA;
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Gietzen D;

Policky JL, Suarez CJ;

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constitute of the invention may have a use in gene therapy. The human clasmostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated to with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorders, gastrointestinal disorders, or disorders, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concerns caused by virus, bacteria, fungi or parasite. The dithp concerns caused by virus, bacteria, fungi or parasite. The dithp concerns caused by virus, bacteria, fungi or semantic molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline concerns of gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pot/en/sequences/listing.htm
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100.0%; Pred. No. 12;
:ive 0; Mismatches
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ne : 54.8125 secs
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Gaps

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100.0%; Score 35; DB 8; Length 111; 100.0%; Pred. No. 6.1; .ive 0; Mismatches 0; Indels

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04; Search time 13.7812 Seconds
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Run on: October 14, 2005, 16:00:04; Search time 13.7812 Seconds (without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513549

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl	Appl	Appl	Appl	Appl	Appl	Appl	App	Appl	Appl	Appl	Appl	AD.	13. Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	4 .6	Ap	Ap,
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		57-1	US-08-652-816A-	025-769B-1	070A-1	53-1	-490-324-19	57-2	840B-			38-1	16-1		-369-364A-	09-025-769B-3	09-025-769B-5	09-490-070A-3	09-490-070A-5	33-33	33-5	24-3	4-5	373B-4	290-17	1A-	-000C-557	-09-134-000C-455
		383-667	52-8	25-7	-490-0	-490-153-1	90-33	33-6	-424-8	-378-939-1	37-5	526-098-1	33-9	-949-016-7	39-3	5-7	12-7	0-0	0-0	90-15	0-16	10-32	0-33			2-99	34-00	4-00
		09-38	9-8	09-0	09-49	09-49	σ	09-383-667-2	09-42	8-37	æ	σ	US-09-383-916-1	9-94	19-36	9-02	9-02	9-49	9-49	US-09-490-153-3	09-490-153-5	09-490-324-3	09-490-324-5	09-247	09-232	9-252	9-13	9-13
	110	ns-c	ns-(us-c	ns-c	ns-c	US-0	ns-c	US-C	us-o	US-0	US-0	ns-c	0S-09	US-09	us-c	US-C	ns-0	ns-0	ns-0	ns-o	us-o	us-0	US-0	US-0	0S-09	US-09-1	ns-0
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	Length	7	111	112	112	112	112	7	7	235	236	236	236	1039	1882	110	110	110	110	110	110	110	110	215	111	140	217	294
	Query	0.0	0.00	0.00	100.0	0.0	0.0	9.6	9.6	88.6	9.6	9.6	9.6	9.6	9.6	7.7	5.7	5.7	2.7	7.	5.7	5.7	5.7	٠		•	0.	0.0
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	Score	35	35	35	35	35	35	31	31	31	31	31	31	31	31	30	30	30	30	30	30	30	30	29	28	28	78	28
	Result No.	1	7	m	4	'n	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 43922, A Sequence 18161, A Sequence 15, Appl Sequence 15, Appl Sequence 23, App Sequence 2, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 17949, A Sequence 23297, A Sequence 23297, A Sequence 22912, A Sequence 22912, A Sequence 22912, A Sequence 22912, A Sequence 3200, A Sequence 32012, A Sequence 32012, A Sequence 32012, A Sequence 22912, A Sequence 23912, A Sequence 3333, Appl Seq
US-09-270-767-43922 US-09-252-991A-18161 US-09-240-136-2750 US-08-867-941-115 US-09-310-9878-2 US-09-310-9878-2 US-09-310-9878-2 US-09-107-5328-11 US-09-107-5328-1296 US-09-248-796A-17949 US-09-270-767-53297 US-09-248-796A-22912 US-09-248-796A-22912 US-09-248-796A-22912 US-09-248-796A-22912 US-09-248-796A-22912 US-09-248-796A-22912
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ALIGNMENTS

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RESULT 1

195-09-381-667-14

1 Sequence 14, Application US/09383667

1 Patent No. 662258

1 General Application US/09383667

1 Patent No. 662258

1 General Application US/09383667

1 Patent No. 662258

1 General Hass Philip E

APPLICANT: Bacon Daniel

APPLICANT: Suggest. Shelly

1 TITE OF INVENTOR THIS BEACH Annual Arti-Pactor IX/IXA Antibodies

1 TITE OF INVENTOR THIS BEACH Annual Arti-Pactor IX/IXA Antibodies

1 TITE OF INVENTOR THIS BEACH Annual Arti-Pactor IX/IXA Antibodies

1 TITE OF INVENTOR THIS BEACH AND NOBER: US/09/383,667

CURRENT FILING DATE: 1999-08-28

1 SARLIER FILING DATE: 1999-08-28

1 SARLIER FILING DATE: 1999-03-03

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ATTORNEY/AGENT INFORMATION
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 DVSKRPS 58
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New York
New York
Y: USA
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  CITY: Ne
STATE: N
COUNTRY:
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                                   STATE: Illinois
CCUWTRY: United States of America
CCUWTRY: United States of America
CCUWTRY: United States of America
CCOMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Datentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/65,816A
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 23-EP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 951064.6
FILING DATE: 02-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 02-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 02-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 02-DEC-1992
PRIOR APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG VILOND WATHA:
APPLICATION NUMBER: US 08/107
FILING DATE: 01-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG WILLOW NUMBER: US 08/107
PRIOR APPLICATION NUMBER: US 08/107
PRIOR APPLICATION NUMBER: US 08/107
PRIOR APPLICATION NUMBER: US 08/244,597
PRIOR APPLICATION NUMBER: US 08/107
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; Sequence 19, Application US/09025769B
; Patent No. 6300664
; GENERAL INFORMATION:
    APPLICANT: Raaplk, Achim
    APPLICANT: Pack, Peter
    APPLICANT: Ge, Liming
    APPLICANT: Plueckhun, Andreas
    TITLE OF INVENTION: Protein/(Foly)peptide libraries
    TITLE OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity ا00..
ابعد 7; Conservative
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TOPOLOGY: li
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COMPUTED: REMABLE FORM:
COMPUTED: REMABLE FORM:
COMPUTED: LIGH FC compatible
SOFTHING DATE: LIGHT-199
FPILOR ADDIES: LIGHT-199
FPILOR DATE: LIGHT-199
FPI
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us-10-614-959-14.raj

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US-09-490-153-19
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US-09-490-153-19
Sequence 19, Application US/09490153
Fatent No. 6706484
Fatent No. 6706484
Fach Timppik, Achim
Fack Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
PlueckInu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMBUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels
      REGISTRATION NUMBER: 31,298
REPREBRUE/DOCKET WUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acide
TYPE: amino acide
                                                                                                                                    | LENGTH: 112 amino acids | TYPE: amino acids | TYPE: amino acid | TYPE: amino acid | STRANDEDNESS: «Unknown> | TOPOLOGY: linear | MOLECTLE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-490-070A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
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MEDIUM TYPE: Floppy disk
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52 DVSKRPS 58
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Patent No. 6828422

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSE:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION DATA:
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
Query Match
100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: 11near; WOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-490-324-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-09-383-667-25
; Sequence 25, Application US/09383667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 112 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                                                          1 DVSKRPS 7
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Same Section

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Sequence 125, Application US/09424840B

Patent No. 6790338

GENERAL INFORMATION:

APPLICANT: Berchtchid, Peter

APPLICANT: Berchtchid, Peter

TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES

FILE REFERENCE: 100564-09049

CURRENT APPLICATION NUMBER: US/09/424,840B

CURRENT FILING DATE: 1999-12-03

PRIOR FILING DATE: 1998-05-08

PRIOR FILING DATE: 1998-12-12

PRIOR FILING DATE: 1997-12-12

PRIOR FILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patentin Version 3.1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT Adams, Camelia W.
APPLICANT Bevaux, Brigitte
APPLICANT Bevaux, Brigitte
APPLICANT Eaton, Dan L.
APPLICANT Hass, Philip E.
APPLICANT JUGICE, J. Kevin
APPLICANT Sugget, Sheller
APPLICANT Kirchhofer, Daniel
APPLICANT Kirchhofer, Daniel
APPLICANT Kirchhofer, Daniel
APPLICANT Kirchhofer, Daniel
APPLICANT INFORMER: US 60/09/383,667
CURRENT APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER PILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
LENGTH: 7
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88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels
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4.1e+05;
0;
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85.7%; Pred. No. 4.1e+05
iive 1; Mismatches
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US-08-378-939-12
Sequence 12, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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pacence 10, Application US/08487550
| Sequence 10, Application US/08487550
| Patent No. 6113898
| GENERAL INFORMATION:
| APPLICANT: Anderson, Darrell R. TITLE OF INVENTION: "MONKEY MONOCIONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: "MONKEY MONOCIONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: IMMUNOSUPPRESANTS"
| TITLE OF INVENTION: IMMUNOSUPPRESANTS"
| NUMBER OF SEQUENCES: 12 CORRESPONDENCE S. 12 CORP. SACKER & MATHIS STREET: 699 Prince Street
| CITYL Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCES: 46
CORRESPONDENCES: ADDRESSEE: SOTHWRLL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRATING SYSTEM: DAIDLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION NUMBER: US/08/487,550 FILMS DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%; Score 31; DB 2;
85.7%; Pred. No. 33;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION 1935

PRIOR APPLICATION 10 0ATA:

APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 1808-118

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6031

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.6
Best Local Similarity 85.7
Matches 6; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-378-939-12
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STATE: VA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22314
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Gaps

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us-10-614-959-14.ra
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Matches

ATTORNEY/AGENT INFORMATION:

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US-09-383-916-10

Sequence 10, Application US/09383916

Sequence 10, 6709654

Parent No. 6709697

Parent N
         2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMUNICATION INFORMATION:
TELEPA: 703-836-6620
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 88.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
   5; Conservative
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MOLECULE TYPE: protein

US-09-383-916-10
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71 DINKRPS 77
                                                                  1 DVSKRPS 7
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US-09-949-016-7859
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/487,550
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                             TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-526-098-10
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71 DINKRPS 77
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Best Local Similarity
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"Sequence 7859, Application US/09949016
Patent No. 6812339
"GENERAL INPORMATION:
TERREAL INPORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
ADDRESSER. ADDRESSER. & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: 0.0 Prince Street
CIUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US(09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INPORMATION:
NAME: TESKIN, ROBIN L.
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Sequence 13, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:

APPLICANT: Hurskainen, Tiina L.

APPLICANT: Hurskainen, Tiina L.

APPLICANT: Hirohat, Satoshi

TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases

TITLE OF INVENTION: 1999-08-06

CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 1882

TYPE: PRT

ORGANISM: Homo sapiens ADAMTS-9
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                                                                                                                                                                                                                                                                                   88.6%; Score 31; DB 4; Length 1039; 100.0%; Pred. No. 1.6e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.6%; Score 31; DB 3; Length 188
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-025-769B-33
is Sequence 33, Application US/09025769B
is Sequence 33, Application US/09025769B
is Patent No. 6300064
is APPLICANT: Knappik, Achim
is APPLICANT: Pack, Peter
is APPLICANT: 1ag, Vic
is APPLICANT: Ge, Liming
is APPLICANT: Plueckthun, Andreas
is TITLE OF INVENTION: Protein/(Poly)peptide libraries
in WIMBER OF SEQUENCES: 373
is CORRESPONDENCE ADDRESS:
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBELSEQ for Windows Version 4.0
SEQ ID NO 7859
LENGTH: 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MOD RES
LOCATION: (468)
OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa = Y
US-09-369-364A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 1 DVSKRP 6
                                                                                                                                                                                                TYPE: PRT
CRGANISM: Human
US-09-949-016-7859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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COMPUTER READABLE FORM:

STATE: New York

STATE: New York

STATE: New York

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: New York

SOFTWARE: New York

SOFTWARE: New York

MEDIUM TYPE: Ploppy disk

MARE: James Flore 198

PRIOR APPLICATION NUMBER: USP

MARE: James F. Haley, JF., Esq.

REGISTRATION NUMBER: 27,794

MEDIUM TYPE MEDIUM TYPE NUMBER: MORPHO/5

TELEPANT INFORMATION:

MEDIUM TYPE NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION
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October 14, 2005, 16:20:10 ; Search time 49.7656 Seconds (without alignments) 58.615 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           OM protein - protein search, using sw model
                                                                                                                                               Run on:
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Title: Perfect score:

US-10-614-959-14 35 1 DVSKRPS 7 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

1859788 Total number of hits satisfying chosen parameters: 1859788 seqs, 416717961 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US11B_W PUB.pep:*
Published_Applications AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Semience 98 April	Semience 98 Anni	Semience 1 Appli	Semience fi anni	Semience 42 Appl	Sequence 1898	Segmence 1808, Ap	Segmente 1030, Ap	Semionce 20ss An	Semience 2000, Ap	Sequence 24, Apply
	4	Q.T.	US-10-308-817-98	US-10-453-698-98	US-10-447-331-1	US-10-360-828-61	US-10-916-758-42	US-09-880-748-1898	US-10-293-418-1898	US-09-880-748-2055	US-10-293-418-2055	US-10-981-692-24	US-10-981-692-40
			15	15	15	15	18	10	15	0	15	18	18
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-09-880-748-192	10-293-418-	-10-981-692-29	-10-981-692-3	-10-981-692-2	-09-880-748-192	-10-293-418-1	-10-293-418-324	-10-981-692	-10-981-692-3	-09-880-748-19	9-880-748-1	-10-293-418-19	-10-293-418-19	-09-880-748-14	-09-880-748-16	-09-880-748-16	-09-880-748-17	-09-880-748-189	19-880-74	-09-880-748-193	-10-293-418-144	-10-293-418-168	5-10-293-418-16	-10-293-418-170	-10-293-418-1	-10-293-418-192	-10-293-418-193	-10-935-290-4	-10-935-290-7	-10-935-290-8	-10-935-290-9	10-935-290-	-10-935-290-1
10	15	18	18	18	10	15	15	18	18	10	10	15	15	10	10	01	10	10	10	10	15	15	15	15	12	15	15	17	17	17	17	17	11
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels
             Squence 98, Application US/10308817
Squence 98, Application US/10308817
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
; SOFTWARE: Patentin version 3.1
; SEG ID NO 98
                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: human
US-10-308-817-98
US-10-308-817-98
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52 DVSKRPS 58 1 DVSKRPS 7 RESULT 2 US-10-453-698-98 ઠે 셤

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Sequence 98, Application US/10453698 Publication No. US20040038308A1 GENERAL INFORMATION APPLICANT: Rother, Russell

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TYPE: PRT
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publication No. US2003020690A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hua, Shaobing

APPLICANT: Zhu, Li

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727

CURRENT FILING DATE: 2003-02-07

PRIOR PELLON NUMBER: US 10/071,866

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR PLING DATE: 2002-02-08

PRIOR PLING DATE: 2002-02-08

PRIOR PLING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

NUMBER OF SEQ ID NOS: 64
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                     Indels
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Sublication No. US2003029434A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Carter, Paul J.

APPLICANT: Carter, Paul J.

TITLE OF INVENTION: DIRACOSIS

TITLE OF INVENTION: DIRACOSIS

TILE REFERENCE: GENENT.122A

CURRENT APPLICATION NUMBER: US/10/447,331

CURRENT FILING DATE: 2000-02-29

PRIOR PILING DATE: 2000-02-29

PRIOR PLING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SECOLD NOS: 6

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                         0; Mismatches
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FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
LENGTH: 99
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Best Local Similarity 100.0
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Matches 7; Conservative
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ORGANISM: Homo sapiens
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CRGANISM: human
US-10-453-698-98
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iSequence 1899, Application US/09880748
j Sequence 1899, Application US/09880748
j Publication No. US20030059937A1
general Involvantion:
j APPLICANT: Ruben et al.
j TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
gile REFERENCE: PFS23
cURRENT APPLICATION NUMBER: US/09/880,748
cURRENT FILING DATE: 2001-06-15
prior FILING DATE: 2000-06-15
prior FILING DATE: 2000-06-15
prior FILING DATE: 2000-10-17
prior FILING DATE: 2000-10-17
prior FILING DATE: 2001-03-16
prior FILING DATE: 2001-03-16
prior PRIOR PAPLICATION NUMBER: 60/277,379
prior PRIOR DATE: 2001-03-16
prior FILING DATE: 2001-03-21
prior FILING DATE: 2001-05-25
j NUMBER OF SEQ ID NOS: 3239
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100.0%; Score 35; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Synthetically generated peptide US-10-916-758-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 35; DB 18;
100.0%; Pred. No. 18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-916-758-42

Sequence 42, Application US/10916758

Sequence 42, Application US/10916758

Publication No. US2050180977A1

GENERAL INFORMATION.

APPLICANT: Madison, Edwin L.

TITLE OF INVENTION ENDOTHELIASE-2 LIGANDS

FILE REFERENCE: 10280-065001

CURRENT FILING DATE: 2004-08-12

PRIOR PILING DATE: 2004-08-12

PRIOR APPLICATION NUMBER: US 60/520,164

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 113

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 42

LENGTH: 118
                                                                                                                                           OTHER INFORMATION: VL of scrv Ab124
US-10-360-828-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
SOFTWARE: PatentIn version 3.1 SEQ ID NO 61 LENGTH: 111 TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100...
7; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1898
LENGTH: 240
                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1898
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ö Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels ઠે

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Gaps

181 DVSKRPS 187 g

RESULT 7

US-10-293-418-1898

Sequence 1898 Application US/10293418

Publication No. US2003022396A1

GENERAL INFORMATION:

APPLICAMT RUDEN

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

CURRENT FILION Antibodies that Immunospecifically Bind BLyS

CURRENT FILION NUMBER: US/10/293,418

PRIOR PPLICATION NUMBER: US/10/293,418

PRIOR PLING DATE: 2001-11-16

PRIOR PLING DATE: 2001-12-19

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2000-03-16

PRIOR PLING DATE: 2000-03-16

PRIOR PLING DATE: 2000-01-17

PRIOR PLING DATE: 2000-01-17

PRIOR PLING DATE: 2000-01-17

PRIOR PLING DATE: 2000-06-16

WUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1898

LENGTH: 240

; TYPE: PRT ; ORGANISM: Homo sapiens US-10-293-418-1898

100.0%; Score 35; DB 15; Length 240; 100.0%; Pred. No. 36; tive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 7; Conservative

ð 원 RESULT 8 US-09-880-748-2055

Sequence 2055, Application US/09880748
Publication No. US2003005993741
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-06-15
PRIOR PLILING DATE: 2000-10-17
PRIOR PLILING DATE: 2000-10-17
PRIOR PLILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN Ver. 2.0 '

ENOTH A. 241 TYPE: PRT ORGANISM: Homo sapiens US-09-880-748-2055

Gaps .. 0 100.0%; Score 35; DB 10; Length 241; 100.0%; Pred. No. 36; tive 0; Mismatches 0; Indele Query Match 100. Best Local Similarity 100. Matches 7; Conservative

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US-10-293-418-2055

i Sequence 2055, Application US/10293418

i Sequence 2055, Application US/10293418

i Publication No. US20030223996A1

i GENERAL INFORMATION:

i APPLICANT: Ruben et al.

i TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

i FILE REPERENCE: PES-23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

i PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/3949

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-103-16

PRIOR PILING DATE: 2000-103-16

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

TYPE: DENTH: 21

; TYPE: PRT ; ORGANISM: Homo US-10-293-418-2055

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 36; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels (

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RESULT 10
US-10-901-692-24
Sequence 24, Application US/10981692;
Sequence 24, Application US/10981692;
Publication No. US20050163777A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REFERENCE: PF590P1
CURRENT APPLICATION NUMBER: US/10/981,692

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RESULT 14
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; Sequence 40, Application No. US20050163777A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2004-11-05
; PRIOR FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICATI'R Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFRENCE: PF23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16
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0
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CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40
                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: NO15E08 scFv
US-10-981-692-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 100...
7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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US-10-981-692-40
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Sequence 29, Application US/10981692
Sequence 29, Application US/10981692
Publication No. US2050163777A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REPERENCE: PFS-90P1
CURRENT APPLICATION NUMBER: US/10/981,692
CURRENT FILING DATE: 2004-11-05
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Sequence 1927, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: RUben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-6-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-17

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                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 35; DB 10; Length 243; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1927
LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                 TYPE: PRT CRGANISM: Homo sapiens US-09-880-748-1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 DVSKRPS 189
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ORGANISM:
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Page 5
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us-10-614-959-14.rapk

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PRIOR APPLICATION NUMBER: PCT/US03/16802
PRIOR FILING DATE: 2003-05-29
PRIOR PELICATION NUMBER: 60/383,802
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
IENGTH: 243
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
PRT
OTHER INFORMATION: N024E07 scFv
US-10-981-692-29
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Query Match
Best Local Similarity 100.0%; Score 35; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189
RESULT 15
US-10-981-692-33
; Sequence 33, Application US/10981692
; Publication No. US20050163377A1

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RESULT 15
US-10-981-692-33
i Sequence 33, Application US/10981692
i Publication No. US20050163777A1
i GENERAL INFORMATION:
i APPLICANT: Rosen et al.
i TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
i TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
i TITLE OF INVENTION UNMER: PF590P1
i CURRENT PILING DATE: 2003-05-29
i PRIOR PILING DATE: 2003-05-29
i PRIOR PILING DATE: 2003-05-29
i PRIOR FILING DATE: 2002-05-30
i NUMBER OF SEQ ID NOS: 76
i SOFTWARE: Patentin version 3.1
i LENGTH: 243
i TYPE: PRT
i ORGANISM: Artificial sequence
i PEATURE: NORMATION: NO23E01 scFv
US-10-981-692-33

Db 183 DVSKRPS 189

1 DVSKRPS 7

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Ouery Match
100.0%; Score 35; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels (

Search completed: October 14, 2005, 17:00:44 Job time : 50.7656 secs

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OM protein - protein search, using sw model

October 14, 2005, 16:02:59 ; Search time 9.73438 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-14 35 1 DVSKRPS 7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

0

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		40			SUMMAKIES	
Result		Query				
Q	Score	Match	Length	8	ID	Description
-	35	100.0	66	7	836057	Id lambda chain
7	34	97.1	646	~	G85056	١.
m	32	91.4	9	~	A24626	Id lambda chain V.
4	32	91.4	103	~	A38923	AL type amyloid fi
S	32	91.4	111	Н	L2HUTR	Id lambda chain V-
φ	32	91.4	423	N	F64690	-
7	31	88.6	110	~	S51149	2
œ	31	88.6	111	7	L2HUWN	lambda chai
σ	31	88.6	111	~	S36281	Jampda
10	30	85.7	112	~	831515	
11	30	85.7	112	7	S44105	Jambda
12	30	85.7	416	7	\$26836	TI eite one
13	29	82.9	74	'n	AH2642	
14	29	82.9	88	~	A97425	hypotherical prote
15	29	82.9	337	-	E70191	
16	29	82.9	377	N	A32548	homeobox protoin w
17	53	82.9	404	2	T00750	nomecond process n
18	29	82.9	685	~	T21466	
19	53	82.9	069	0	T21806	hypothetical prote
20	59	82.9	735	2	T00850	nypochecical proce
21	29	82.9	972	۱۵	H84903	
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3 6	N (1101	7	DORTZI	hypothetical prote
57	67	82.9	1245	~	G84897	hypothetical prote
25	28	80.0	91	N	T09711	ADP. ATP carrier or
56	28	0	111	,-4	L2HUMC	
27	28	ö	189	~	AE1316	cvclohydrola
28	28	80.0	189	~	AE1688	
53	28	80.0	235	N	S25759	_

Ig lambda chain - 60s ribosomal prot hypothetical prote hypothetical prote probable lipoprote hypothetical prote mutants block spor thioredoxin reduct thioredoxin reduct thioredoxin reduct familial Alzheimer SRPMS4 protein - M	hypothetical prote gene 12 protein - 4-hydroxybutyryl-C pseudolysin (EC 3.
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1g lambo C;Specie C;Date:	1g Iambda chain - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text change 21-Jan-2000
C;Access R;Willia	C;Accession: S36057 - C:R;Williams, S.C.
submitte A;Refere	submitted to the EMBL Data Library, April 1993 A;Reference number: S36046
A;Access	A; Accession: S16057
A; Status A; Molecu	A; Status: preliminary A; Molecule type: DNA
A; Cross-	ce: 1-35 <4115 references: EMBL:Z22198; NID:G312319; PIDN:CAAR020R.1: PID:G11212
C;Superf C;Keywor	C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-92/	Domain: immunoglobulin homology <imm></imm>
Query Best L	tch al Similarity 100.0%; Score 35; DB 2; al Similarity 100.0%; Pred. No. 1.1;
Macches	s /; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
o _y	1 DVSKRPS 7
Dp	52 DVSKRPS 58

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		kinase	
		protein	
		receptor-like	Charles and the second
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RESULT 2
G85056
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C;Accession: G85056
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Tile: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Accession: G85056
A;Status: preliminary
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Residues: 1-646 <STO>
A;Cross-references: UNIPROT:Q9XEC7; GB:NC_001268; NID:g7267207; PIDN:CAB77918.1; GSPDB:G7
C;Genetics:
A;Genetics:
A;Genetics:
A;Gaperfamily: protein kinase homology

ô Gaps ô Query Match 97.1%; Score 34; DB 2; Length 646; Best Local Similarity 85.7%; Pred. No. 12; Matches 6; Conservative 1; Mismatches 0; Indels

1 DVSKRPS 7

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antibody light chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
A;Reference number: S5147
A;Reference number: S5147
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             A;Cross_references: GDB:119342; OMIM:147240
A;Cross_references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; C;Complex: An immunoglobulin heterotetramer such as IgA and IgM, the subunits associate into landant disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into landar disultive immunoglobulin vegion; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology < IMM> < IMMO </li>
F;1/Modified site: blocked amino end (Gin) (probably pyrrolidone carboxylic acid) #statut
F;2-90/Disulfide bonds: #status predicted
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A;Cross-references: EMBL:X83712
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 110
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Pred. No. 9.8;
1; Mismatches
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Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 1;
Pred. No. 5.9;
1; Mismatches
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85.7%;
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85.7%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.71
Matches 6; Conservative
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EVSKRPS 56
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A;Residues: 1-110 <DEK>
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A;Gene: GDB:IGLV@
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R;Eulitz, M.; Linke, R.P.
Bicchem. Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
A;Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amyl A;Reference number: A38923; MUID:93356823; PMID:8352801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig lambda chain V-II region (Tro) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Species: 9-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01973
R;Scholz, R.; Yang, C.; Hilschmann, N.
R;Scholz, R.; Yang, C.; Hilschmann, N.
A;Title: Zur Strukturregel drem 360, 1903-1918, 1979
A;Title: Zur Strukturregel drem Antikoerper. Die Primmerstruktur eines monoklonalen IgA
A;Reference number: A01973; MUID:80114123; PMID:118915
                                                                                                                                                                                                                                             Ig lambda chain V-II region (Har) - human (fragment)
Ig lambda chain V-II region (Har) - human (fragment)
Ig lambda chain V-II region (man)
C;Deceles: Hone: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C;Accession: A24626
R;Eulitz, M.; Linke, R.
Biol. Cham. Hoppe-Seyler 366, 907-915, 1985
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a A;Reference number: A24626; MUID:86077295; PMID:3935132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Accession: A38923
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C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
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A;Residues: 1-60 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-111 <SCH>
A;Cross-references: UNIPROT:P01707
C;Comment: This chain was isolated from a myeloma protein.
C;Genetics:
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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|DVNKRPS 49
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A38923

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us-10-614-959-14.rpr

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submitted to the EMBL Data Library, January 1993
A;Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody final A;Reference number: 831515
A;Recession: 831515
A;Accession: S31515
A;Status: preliminary
A;Rotlus: preliminary
A;Residues: 1-112 <VAN>
A;Residues: 1-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Januara Ciratin V. Legucia - Indiana.
C; Species Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C; Accession: 84-105
C; Accession: 84-105
C; Accession: 84-105
C; A; Emblin, T.J.; Stevenson, F.K.
C; Hawkins, R. B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
C; Hawkins, R. B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
C; Hawkins, R. B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
C; Stetus: preliminary
A; Reference number: 844-105
A; Residues: 1-112 < HAW>
A; Residues: 1-112 < HAW>
A; Residues: 1-112 < HAW>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-92/Domain: immunoglobulin homology < INM>
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A;Cross-references: UNIPROT:P23191; EMBL:X56977; NID:g44180; PIDN:CAA40298.1; PID:g44182
C;Keywords: hydrolase
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85.7%; Pred. No. 17;
ive 0; Mismatches
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Pred. No. 17;
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1; Mismatches
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Ig lambda chain V-J region - human
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Best Local Similarity 85.73
Matches 6; Conservative
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Best Local Similarity 85.7;
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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A;Gross-references: GDB:119342; OMIM:147240
A;Map position: 22411.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology immunoglobulin homology
F;15-92/Domain: immunoglobulin homology immy
F;15-92/Domain: immunoglobulin homology immy
F;15-90/Disulfide bonds: #status predicted
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Rs. Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. A.Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MuID:93178448; PMID:7679990
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                                                                                                         Ig lambda chain V-II region (Win) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Species: Homo sapiens
C;Species: Allow Single Sequence revision 30-Nov-1979 #text_change 09-Jul-2004
C;Species: A.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.
Biochim. Biophys. Acta 537, 9-21, 1978
A;Reference and sequence of the human myeloms lambda chain Win.
A;Reference number: A01978; MUID:79062503; PMID:102365
A;Residues: 1-111 <CHE>
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ug lambda chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31515
R;van der Heijden, R.W.J.; Uytdehaag, F.G.C.M.; Osterhaus, A.D.M.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 1;
Pred. No. 9.9;
0; Mismatches 1
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Pred. No. 9.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P01712
C;Comment: This is a Bence Jones protein.
C;Genetics:
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85.7%;
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Best Local Similarity 85.7%;
Matches 6; Conservative 1
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EVSKRPS 58
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Matches
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141 NISKRPS 147
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C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: E70491
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
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C;Species: 30-Sep_2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT:Q8UHW8; GB:AE007869; PIDN:AAK86354.1; PID:g15155478; GSPDB:q
hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11.7an-2002 #sequence_revision 11.7an-2002 #text_change 09.Jul-2004 C; Accession: AH2642 J. C; Kaul, R: Monks, D:; Chen, L:; Wood, G.E.; Chen, Y:; Woo, I R; Wood, D.W.; Setubal, J.C.; Kaul, R: Monks, D:; Chen, L:; Wood, G.E.; Chen, Y: Woo, I R; Wood, D:; Chen, L:; Wood, G.E.; Chen, Y:; Woo, I Fxarp, P: Romero, P: Zhang, S. Science 294, 2317-2323, 2001 ** Ahathors: Yoo, H:; Tao, Y: Biddle, P:; Jung, M:; Krespan, W:; Perry, M:; Gordon-Kamm, And Thors: Yoo, H:; Tao, Y: Biddle, P:; Jung, M:; Krespan, W:; Perry, M:; Gordon-Kamm, And Thors: Yoo, H:; Tao, Y: Biddle, P:; Jung, M:; Krespan, W:; Perry, M:; Gordon-Kamm, And Thors: Yoo, H:; Tao, Y: Biddle, P:; Jung, M:; Krespan, W:; Perry, M:; Gordon-Kamm, And Thors: Yoo, H:; Tao, Y: Biddle, P:; Jung, M:; Krespan, W:; Perry, M:; Gordon-Kamm, And Tao, Y: Biddle, P:; Jung, M:; Krespan, W:; Perry, M:; Gordon-Kamm, And Tao, Y: Biddle, P:; Jung, W:; Frespan, W:; Frespan, W: Frespan, W: Frespan, W: Frespan, W: Frespan, W:; Frespan, W: Fr
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.
Ajtlil: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2642
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Pred. No. 19;
1; Mismatches 1; Indel8
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
Molecule type: DNA
Residues: 1-74 <KUR>
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Nature 390, S80-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: 170191
A;Accession: 170191
A;Molecule type: DNA
A;Residues: A.ST. eKLE>
A;Acsesicus: J.33 **CKLE>
A;Acsesicus: J.33 **CKLE>
A;Acses-references: UNIPROT:051676; GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AAC67081
A;Experimental source: strain B31
C;Superfamily: translation factor, SUAS type

ö Gaps ; 0 Query Match 82.9%; Score 29; DB 1; Length 337; Best Local Similarity 71.4%; Pred. No. 88; Matches 5; Conservative 2; Mismatches 0; Indels

Search completed: October 14, 2005, 16:23:40

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OM protein - protein search, using sw model

October 14, 2005, 15:51:44; Search time 46.5938 Seconds (without alignments) 76.932 Million cell updates/sec Run on:

US-10-614-959-14 35 1 DVSKRPS 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	09xec7 arabidonala		рошо	helic				_	-	Q82893 streptomyce	_			homo se				homo		buchn		_		Q86v04 homo sapien	enchy	Q7s098 neurospora	O6dhx1 homo sapien	P23191 moraxella b	Q80u48 mus musculu	Q6phc0 mus musculu	mus
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Q9DBJ2 TM24 HUMAN TM24 MOUSE Q6DDL7 Q6DDL7 Q6AQQ1 Q8CQ01 Q8SX99 Q9VN46 Q6EXY3 Q8EXY3 Q8EXY3 Q8UHW8 Q6EXQC
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last annotation update)
17-Stock (TrEMBLrel. 27, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                          Score 34; DB 2; Length 646;
Pred. No. 69;
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Pyrrolidone carboxylic acid.
By similarity.
                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0006955; P: 1 mmunne response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR0047; Ig; 1.
SWART; SM0046; Ig; 1.
PROSITE; PS50815; IG_LIKE; 1.
PROSITE; PS50815; IG_LIKE; 1.
Procite in sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid.
Ig-like.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
10 lambda chain V-II region TRO.
Homo sapiens (Human).
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                               97.1%;
85.7%;
          Query Match
Best Local Similarity 85.77
Conservative 6;
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                                                                                                                                                                                     606 DISKRPS 612
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52 DVTKRPS 58
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A
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05-JUL-2004 (
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D1D Q6P107
D1 O5-J0
D1 O5-J0
D1 O5-J0
D2 O5-J0
D3 O5-J0
D4 O5-J0
D5 O5-J0
D6 O5-J0
D7 O5-J0
D7 O5-J0
D8 O5-J0
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Riachull S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Rab Jatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab Jatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab Stapleton M., Soares M.B., Bonaldo M.F., Gaarvant T.L., Scheetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards B., Worley W.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakebley B. W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

R. Todeneration and initial analysis of more than 15,000 full-length human
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STRAIN=26695 / ATCC 700392;
MEDLINE=971394467; PubMed=9252185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleistachmann R.D., Kerchum K.A., Klent H.-P., Gill S.R., Kirkness E.F.,
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Zhou L.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type IIS restriction enzyme R protein (MBOIIR).
OrderedLocusNames=HP1366;
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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TISSUE-Lung;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0309983; AAH30983.1; -.
HSSP; P01709; 1A8J.
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SEQUENCE 236 AA; 25021 MW; 4A07BEF60A5FD465 CRC64;
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Interpro; IPR003199; Ig.
Interpro; IPR00110; Ig-like.
Interpro; IPR003106; Ig-MC.
Interpro; IPR003596; Ig-MC.
Interpro; IPR003596; Ig-W.
Interpro; IPR004596; Ig-W.
SWART; SW00409; IG-2.
SWART; SW00409; IG-2.
PR0SITE; PS00390; IG-LIKE; 2.
PROSITE; PS00290; IG-LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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NCBL_TaxID=210;
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Q7MUS6

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DOI=10.1128/JB.185.18.5591-5601.2003; Melson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Elsen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Melson W.C., Mason T.M., Tallon L., Gray J., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst R.E., Fraser C.M., "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
                                                       Q7MUS6 PRELIMINARY; PRT; 130 AA.
Q7MUS6;
Q7MUS6;
Q7MUS6;
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myorbtetical protein.
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pyorbtetical protein.
PortediocusNames=FG1409;
Porthyromonas gingivalis (Bacteroides gingivalis):
Bacteroidetes; Bacteroides
Bacteroideses; Porthyromonas
NCBI_TAXID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein.
SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23E5805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22829867; PubMed=12949112;
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Best Local Similarity 71.44;
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107 DISRRPS 113
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-1- SIMILARIY: Contains I immunoglobulin-like domain. PIR; A01978; LZHUWN.

RSSP; PO1709; LZHUWN.

RSSP; PO1709; LZHUWN.

RSSP; PO1709; LZHUWN.

RSSP; PO1003823; Frantigen binding; NAS.

GO; GO:0005855; P:immuno response; NAS.

RO; GO:0006855; P:immuno response; NAS.

RITHEPTO; IPR00110; Ig-like.
Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Waldman J.F., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C., "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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85.7%; Pred. No. 53;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA; 50047 MW; 9086E51C8FE4E58E CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-II region WIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA
                                                                                                                                                                                                                                                                                            EMBL; AE000637; AAD08410.1; -.
PIR; F64690; F64690.
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InterPro; IPR003615; HNH_nuc.
SMART; SM00507; HNHC; 1.
                                                                                                                                                                                                                      pylori.";
Nature 388:539-547(1997)
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Best Local Similarity 85.7
Matches 6; Conservative
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71 DMSKRPS 77
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88.6%; Score 31; DB 2; Length 130; 71.4%; Pred. No. 63; 1.4%; Pred. 2; Mismatches 0; Indels

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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., Fitzelugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
B. Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Oui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Natrig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freiteg M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
T. The Genome Sequence of the Filamentous Fungus Neurospora crasss.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                        Last sequence update)
Last annotation update)
         233 AA.
                                                   Created)
       PRT;
0754H3 PRELIMINARY;
0754H3 0
01-MAR-2004 (TERBLEEL 26, L6
01-MAR-2004 (TERBLEEL 26, L6
01-MAR-2004 (TERBLEEL 26, L6
Hypothetical protein.
                                                                                                                                                                Neurospora crassa.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Gaps

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DVDKRPS 58 1 DVSKRPS 7

25

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Gaps

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Q7SZL9

RESULT 8 Q7SZL9

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SYNCHARTS

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Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N., Kuwahara T., Hattori M., Hayashi T., Ohnishi Y.; Hattori M., Hayashi T., Ohnishi Y.; "Genomic analysis of Bacteroides fragilis reveals extensive DNA inversions regulating cell surface adaptation."; Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004). EMBI, AP006841; BAD48181.1; SEQUENCE 402 AA; 45596 MW; 2D56AGDAF87797CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermithis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa H., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
                                      Bacteroides fragilis.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=817;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.6%; Score 31; DB 2; Length 402; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0359; BP450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Complete proteome; Heme; Moncoxygenase; Oxidoreductase.
SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;
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-!- SIMILARITY: Belongs to the cytochrome P450 family.

EMBL; AP005047: BAC74417.1; -.

GO; GO:0004497; F:monooxygenase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR002397; BP450.

InterPro; IPR001288; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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85.7%; Pred. No. 2.5e+02;
Predicted nucleoside-diphosphate sugar epimerase.
ORFNames=BF1430;
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Name=cyp24; OrderedLocusNames=SAV6706;
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MEDLINE=22608306; PubMed=12692562;
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Matches 6; Conservative
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SEQUENCE FROM N.A.
STRAIN=YCH46;
Yamash
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Best Local Similarity
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Q828G3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP-gated ionotropic P2X receptor subunit 2.
Name-p21x2; Synonyms=p2xr2;
Name-p21x2; Synonyms=p2xr2;
Barachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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        preliminary data.

EMBL; AABX01000366; EAA30397.1; -.

EMBL; AABX01000366; EAA30397.1; -.

GO; GO:0015035; C:periplasmic space (sensu Gram-negative Bact. ..

GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.

InterPro; IPR010895; DSBA.

InterPro; IPR010996; DSBA.

InterPro; IPR010996; DSBA.

Hypothetical protein.

EGUENCE 233 AA; 25367 MW; 5088F4A369168929 CRC64;
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                                                                                                                                                                                                                                                                                               Query Match

88.6%; Score 31; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                          11 protein.
233 Aa; 25367 MW; 50B8F4A369168929 CRC64;
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Matches 6; Conservative
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NCBI TaxID=7955;
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25-OCT-2004
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25-OCT-2004
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RESULT 14 엄 à g ö ö SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

Gallogan U.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

A Jaffe D., FitzHugh M., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

RIKINS T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

A Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

A Ram M., Kamvysgelis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

Cogoni C., Macino G., Catcheside D. Li W., Pratt R.J., Osmani S.A.,

DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

Natvig D.O., Alex L.A., Mannhaut G., Ebbole D.J., Freitag M.,

Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,

"The Genome Sequence of the Filamentous Fungus Neurospora crassa."; Gaps Gaps PubMed=14665450; DOI=10.1128/EC.2.6.1151-1161.2003; Catlett N.L., Yoder O.C., Turgeon B.G.; "Mhole-genome analysis of two-component signal transduction genes in Nature 0:0-0(2003).

-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABX01000022; EAA35484.1; -.

SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64; ö Neurospora crassa. Eukaryota, Fungi, Ascomycota, Perizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora. ö Cochliobolus heterostrophus (Drechslera maydis), Eukaryota, Fungi, Ascomycota, Pezizomycotina, Dothideomycetes; Pleosporales, Pleosporaceae; Cochliobolus. 88.6%; Score 31; DB 2; Length 728; 85.7%; Pred. No. 3.8e+02; ive 0; Mismatches 1; Indels 0; Indels Created) Last sequence update) Last annotation update) Q6SLD6; 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) PRT; 1292 AA Putative histidine kinase HHK11p. 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, PRELIMINARY; Local Similarity 85.7 PRELIMINARY; 428 DVSQRPS 434 336 DASKRPS 342 1 DVSKRPS 7 Predicted protein. Name=NCU00559.1; 1 DVSKRPS 7 SEQUENCE FROM N.A. NCBI_TaxID=5141; Name=HHK11; STRAIN=C4; RESULT 11 Q7SF90 ID Q7SF90 AC Q7SF90; Query Match 9GIS90 Best Loca Matches RESULT 12 ... qa ઠે ò g

RT fungal pathogens.";

RL = kwaryotic Cell 2:1151-1161(2003).

CC = 1- SIMILARITY: Concains 1 hietidine kinase domain.

BR G: GO:0016020; C:membrane; IEA.

BR GO: GO:001524; F:ATP binding; IEA.

GO: GO:0003524; F:ATP binding; IEA.

BR GO: GO:000156; F:kuo-component response regulator activity; IEA.

BR GO: GO:000156; F:kuo-component response regulator activity; IEA.

BR GO: GO:000156; F:kuo-component response regulator activity; IEA.

BR GO: GO:000156; F:kuo-component sagnal transduction system (p. .; IEA.)

BR GO: GO:000166; P:kuo-component signal transduction system (p. .; IEA.)

BR GO: GO:000166; F:kuo-component signal transduction system (p. .; IEA.)

BR GO: GO:000166; F:kuo-component signal transduction system (p. .; IEA.)

BR GO: GO:000166; F:kuo-component signal transduction system (p. .; IEA.)

BR GO: GO:000166; F:kuo-component signal transduction system (p. .; IEA.)

BR InterPro: IPR001789; Response reg.

BR Fam; PF00512; His kinase.

BR Fam; PF00139; His kinase.

BR SWART; SM00344; BCTRESENSOR.

BR SWART; SM00389; His kinase.

BR SWART; ö ö Gaps Gaps Ashbya gossypii (Yeast) (Eremothecium gossypii). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Eremothecium. NCBI_TaxID=33169; ö STEAIN-ATCC 10895;
Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Philippen P.,
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016815; AAS50638.1; -.
AGD; ABL133C; -.
SEQUENCE 1766 AA; 179132 MW; BEC73A1CF69F2EA3 CRC64; ö Query Match
88.6%; Score 31; DB 2; Length 1292;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels / Match 88.6%; Score 31; DB 2; Length 1766; Local Similarity 85.7%; Pred. No. 9.6e+02; les 6; Conservative 1; Mismatches 0; Indele Q75E06; 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) PRELIMINARY; |||:||| 1445 DVSERPS 1451 45 DVDKRPS 51 1 DVSKRPS 7 1 DVSKRPS 7 SEQUENCE FROM N.A. ORFNames=ABL133C; ABL133Cp. Query Match Q75E06 RESULT 13 Q75E06 Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and versican.

CATALYTIC ACTIVITY: Cleaves aggrecan at the 1838-Glu-|-Ala-1839 site and versican at the 1428-Glu-|-Ala-1429 site.

1. COPACTOR: Binds 1 zinc ion per subunit (By similarity).

1. SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

2. ALTERNATIVE PRODUCTS:

B. FOALL-Alternative pplicing; Named isoforms=3;

Name=1; Synonyms=ADAMTS-9B;

Isold=Q9P2N4-3; Sequence=Displayed;

Name=2; Synonyms=LADAMTS-9B;

Isold=Q9P2N4-1; Sequence=USP 007548, USP 007549;

Note=May result from the retention of an intron in the cDNA note=May result from the retention of an intron in the CDNA note=May result from the retention.

C leading to a prematurate stop codon;

Name=3; Synonyms=Short;

C leading to a prematurate stop codon;

C leading to a prematurate stop codon;

C RENTESSE SPECIFICITY: Highly expressed in all fetal tissues.

C PATESUE SPECIFICITY: Highly expressed in all fetal tissues.

C PATESUE SPECIFICITY: Highly expressed in all fetal tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heart, placenta and skeletal muscle.
DOMAIN: The spacer domain and the TSP type-1 domains are important
for a tight interaction with the extracellular matrix (By
                                                                                                                                                                                                                                                                  a novel member of the ADAM-TS/Metallospondin gene family.";
                                                                                     metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20181126; PubMed=10718198;
Nagage T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVI.
The complete sequences of 150 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for large proteins in vitro.";
DNA Res. 7:65-73(2000).
-!- FUNCTION: Cleaves the large aggregating proteoglycans, aggrecan
                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
MEDLINE=22513925; PubMed=12514189; DOI=10.1074/jbc.M211009200;
Somerville R.P., Longpre J.-M., Jungers K.A., Engle J.M., Ross M.,
Evanko S., Wight T.N., Leduc R., Apte S.S.;
Evanko S., Wight T.N., LabAnts-9 and ADAMTS-20 as a distinct ADAMTS
subfamily related to Caenorhabditis elegans GON-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
DOMAIN: The ancillary domains, including the TSRs domain, are
required for specific extracellular localization and for its
                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         versicanase and aggrecanase activities.
PTM: The precursor is cleaved by a furin endopeptidase (By
                                                                                                                                                                                                                          MEDLINE-20396138; PubMed=10936055; DOI=10.1006/geno.2000.6246; Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A. Maki R.A.; a novel member of the ADAM-TS/Metallospondin gene f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the peptidase M12B family.
-!- SIMILARITY: Contains 1 disintegrin-like domain.
-!- SIMILARITY: Contains 1 GON domain.
-!- SIMILARITY: Contains 15 TSP type-1 domains.
                    ATS9_HUMAN STANDARD; PRT; 1935 AA.

Q9P2N4; Q9NR29;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
ADAMT6-9 precursor (EC 3.4.24.-) (A disintegrin and me with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).

Name-ADAMT69; Synonyms=KIAA1312;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2).
                  PRT; 1935 AA
                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 278:9503-9513(2003).
                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3) TISSUE=Fetal;
                                                                                                                                                                                                                                                                                       Genomics 67:343-350(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and versican.
                                                                                                                                                                        NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
        ATS9
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                DR Genew; HGNC:13202; ADAMTS9.

DR Genew; HGNC:13202; ADAMTS9.

MIN, 60:6421; ---

DR GO; 20:0008217; F:metallopeptidase activity; TAS.

GO; GO:0008516; P:glycoprotein catabolism; TAS.

DR GO; GO:000516; P:glycoprotein catabolism; TAS.

DR GO; GO:000516; P:glycoprotein catabolism; TAS.

DR GO; GO:000516; P:glycoprotein catabolism; TAS.

DR InterPro; IPR010294; ADAM spacer1.

DR InterPro; IPR00189; Pept M.ZB.

DR InterPro; IPR00189; Pept M.ZB.

DR InterPro; IPR00189; Pept M.ZB.

DR InterPro; IPR00189; Peptidase_M12B.

DR InterPro; IPR001894; TSP1.

DR Ffam; PF01562; Pep M.ZB propep; 1.

DR Pfam; PF01562; Pep M.ZB propep; 1.

DR Ffam; PF01562; Pep M.ZB propep; 1.

DR Pfam; PF01562; Pep M.ZB propep; 1.

DR PROSITE; PS00164; CYSTEINE SWITCH; FALSE_NEG.

DR PROSITE; PS00142; TSP1; 14.

DR PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROPER PROSITE; PS00142; ZINC PROTEASE; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

PROPER PROSITE; PS00142; ZINC PROTEASE; 1.

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PROPER PROSITE; PS00142; ZINC PROTEASE; 1.
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Disintegrin-like.
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TSP Cype-1 11.
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                                                                                                                                                                              EMBL; AF261918; AAF89106.1; -. EMBL; AF488803; AAO15765.1; -. EMBL; AB037733; BAA92550.1; -. HSSP; P07996; 1L5L.
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COOT 57.55.07

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N-linked (GlcNAc. . .) (Potential).
CLVTCGKGH -> VRWEGCYFP (in 1soform 3).
/FTId=VSP_005499.
                                                                                                           | Missing (In isoform 3). |
| Frid=VSP_00550. |
| CSVTGG -> VPSWEL (in isoform 2). |
| Frid=VSP_00550. |
| Frid=VSP_00550. |
| Frid=VSP_007549. |
| Frid=VSP
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Gaps ö 88.6%; Score 31; DB 1; Length 1935; 100.0%; Pred. No. 1.18+03; 1ve 0; Mismatches 0; Indels Query Match Best Local Similarity 100.

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|||||| 1596 DVSKRP 1601

• STANDARD; BFR1 MAGMG OS0171; RESULT 15

BFR1 MAGMG

DC 0501711

DT 15-JUL

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164 AA

Magnetospirillum magnetotacticum (Aquaspirillum magnetotacticum) Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospirillum. 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Bacterioferritin subunit 1 (BFR 1).

SEQUENCE PROM N.A. STRAIN=MS-1

MEDLINE-9872426; PubMed-9409768; DOI=10.1016/S0378-1119(97)00424-1; Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.; "Evidence for two types of subunits in the bacterioferritin of Magnetospirillum magnetotacticum.";

Gene 201:31-36(1997).
-1- FUNCTION: May perform analogous functions in iron detoxification and storage to that of animal ferritins (By similarity).
-1- COFACTOR: Binds 1 heme b (iron-protoporphyrin IX) group per

monomer (Potential).
--- SUBUNIT: Oligomer of 24 identical subunits (By similarity).
--- MISCELLANBOUS: The di-iron binding site functions as active site where iron ions are oxidized from iron(II) to iron(III) before they are stored (By similarity).
--- SIMILARITY: Belongs to the bacterioferritin family.
--- SIMILARITY: Contains 1 ferritin-like diiron domain.

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InterPro; IPR002024; Bacterioferritin. InterPro; IPR009078; Ferritin/RR like. InterPro; IPR008331; Ferritin_Dps. EMBL; AF001959; AAC91253.1; -.

InterPro; IPR09040; Ferritin_like Pfam; PF00210; Ferritin; 1. PRINTS; PR00601; BACFERRITIN.

Iron 1 (By similarity).
Iron (heme axial ligand) (Potential).
Iron 1 (By similarity).
Iron 2 (By similarity). Probom, PD002269; Bacterioferritin; 1.
TIGREAMS; TIGR00754; bfr; 1.
PROSITE; PS00549; BACTERIOFERRITIN; 1.
PROSITE; PS0055; FERTIOFINE; 1.
Heme; Iron; Iron storage; Metal-binding.
DOMAIN 1 1 147 18491 MW; 18 51 51 51 12 54 13 13 13 13 13 METAL SEQUENCE METAL METAL METAL METAL METAL METAL METAL

Gape ö Score 30; DB 1; Length 164; Pred. No. 1.4e+02; 1; Mismatches 0; Indels 85.7%; 5; Conservative Best_Local Similarity Matches 5; Conserv Query Match

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Search completed: October 14, 2005, 16:19:57 Job time : 48.5938 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

using sw model protein search, protein δ

October 14, 2005, 15:51:19; Search time 84.5625 Seconds (without alignments) 50.310 Million cell updates/sec Run on:

US-10-614-959-15 58 Title: Perfect score:

1 AAWDDSLSEFL 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
3: geneseqp200s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2001s:*
7: geneseqp2003s:*
8: geneseqp2003s:* geneseqp2000s;* geneseqp2001s;* geneseqp2003as;* geneseqp2003as;* geneseqp2003bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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SUMMARIES	ID	AAY79073	AAR80087	AAW95485	AAU02544	AAU02558	AAU02612	AAU02627	AAU02629	AAW19883	AAU02542	AAU02551	AAU02585	AAU02606	ADG34301	ADG34317	ABP45916	ADG96743	ADG34310	ADG34306	ADG34303	ABP45915	ADG96742	ADG98057	ADE83862	ADG34308
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æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	28	28	28	28	28	58	28	28	28	28	28		28	28	28	28	28	28	28	28	28	28	28	28	28
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Abp45902 Human BLy Abp45906 Human BLy Adg96733 Single ch Adg96723 Single ch Adg96733 Single ch Adp4591 Human BLy Abp45921 Human BLy Abp45921 Human BLy Abp45921 Human BLy Abp45921 Human BLy Abp4591 Human BLy Abg4596 Human BLy Adg30415 Single ch Adg96715 Single ch Adg96759 Single ch	
ABP45902 ABP45906 ABP45906 ADG96733 ADG96729 ABP45432 ABP45917 ABP45917 ABP45886 ABP45888	ADE83874
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45

ALIGNMENTS

AAY79073 standard; peptide; 11 AA.

AAY79073;

12-JUN-2000 (first entry)

Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence

Complémentarity determining region 3, CDR3; antibody; Gla domain; factor IX/IXa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary arter; bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PTCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC. AAY79073
ID AAY7
XX
XX
AAY79073
XX
DT 12-J
DX 12-J
DX 12-J
DX AAY7
XX
COMP
KW ATTE
XX
COMP
KW

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

99WO-US019453. 26-AUG-1999;

98US-0098233P. 99US-0122767P. 28-AUG-1998; 03-MAR-1999;

(GETH) GENENTECH INC

Kirchhofer D; Judice JK, Навв РЕ, Devaux B, Eaton DL, Adams CW, Suggett S;

"PI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.

Claim 8; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of the light chain variable domain of a human anti-factor IX/IXa Gla domain anti-body. Factor IXa is a vitamin K dependent plasma serime procease that participates in the blood coaqulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo

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the treatment or prophylaxis of thrombotic or coagulopathic diseases or disorders in a mammal for which inhibiting a FIX/IXa mediated event is indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable angina, post myocardial infarction, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal coronary angioplasty (PTCA), stroke, tumour growth, invasion or metaetesis, inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS), arterial fibrillation and disseminated intravascular coagulopathy (DIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of catalytic antibodies displayed on phage - by generating gene library of antibody-derived domains and expressing it in phage
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    Light chain; RT3; human; catalytic antibody; bacteriophage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region
                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiswell D, Darsley MJ, Titmas RC, Williams RO;
                                                                                                                                                                   100.0%; Score 58; DB 3;
100.0%; Pred. No. 0.0022;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                             Human derived light chain RT3 phage antibody.
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/note= "framework region 4"
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e= "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                        AAR80087 standard; protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccafferty J,
Martin MT,
                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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/note=
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                                                                                                                                              Sequence 11 AA;
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Region
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The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                        Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFV; RT3.
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                               Human-derived RT3 phage antibody light chain genetic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martin MT;
                                                                                                                   100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.023; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fitzgerald K, Darsley MJ, Williams RO, Smith R, Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
                                                                                                                                                                                                                                                                                AAW95485 standard; protein; 104 AA.
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                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                               1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCCAFFERTY J.
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MARTIN M T.
KENTEN J H.
SMITH R.
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DARSLEY M J.
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                                                                                               Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                            AAW95485;
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(CHIS/)
(DARS/)
(TITM/)
(MART/)
(KENT/)
(SMIT/)
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Disclosure, Fig 20; 133pp; English

vectors.

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antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. Sequences AAW95484-489 represent genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage
                                                                                                                                    100.0%; Score 58; DB 2; Length 104; 100.0%; Pred. No. 0.023; 1.1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                          Anti-adipocyte monoclonal antibody light chain, FAT 31
                                                                                                                                                                                                                                                          AAU02544 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                1 AAWDDSLSEFL 11
                                                                                                                                                                                             antibody library
                                                                                                               Sequence 104 AA;
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Gaps

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11-OCT-2000; 2000WO-GB003900. 19-APR-2001

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

12-OCT-1999;

Vaughan TJ Edwards BM, Main SH,

WPI; 2001-282031/29. N-PSDB; AAS03444.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid Claim 1; Page 120; 182pp; English diseases

records of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of beastry and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody of an used as therspeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a cetectable label such as radioclabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-

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                                                                                                                                                                                                                  fat;
                                      Length 109;
                                   100.0%; Score 58; DB 4; Length 10
100.0%; Pred. No. 0.024;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                              Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                            Anti-adipocyte monoclonal antibody light chain, FAT 44
abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                      AAU02558 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                 11-OCT-2000; 2000WO-GB003900
                                                                                                                                                                                                                                                                                                                  12-OCT-1999; 99US-0158812P.
                                                                                                                                                                           (first entry
                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                  90 AAWDDSLSEFL 100
                                                                         1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                      Edwards BM, Main SH,
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                   Sequence 109 AA;
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                                                                                                                                                                           29-AUG-2001
                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                         AAU02558;
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ID AAU
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used to deliver drugs or
concluys directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
confidence of adipocyte artigles. Antibodies may be labeled with a
cused in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
contraction than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intracontraction.

Claim 1; Page 128-129; 182pp; English.

diseases.

Sequence 110 AA;

ö Gapa ô Query Match 100.0%; Score 58; DB 4; Length 110; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 11; Conservative 0; Mismatches 0; Indels

AAU02627;

1 AAWDDSLSEFL 11

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Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                               Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                               Anti-adipocyte monoclonal antibody light chain, FAT 99
                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                               AAU02612 standard; protein; 110 AA
                                                                                                                                                                                                                                             Vaughan TJ;
                                                                                                                                                                                                                                                                                                                        Claim 1; Page 163; 182pp; English.
                                                                                                                                                                                           11-OCT-2000; 2000WO-GB003900.
                                                                                                                                                                                                             99US-0158812P
                                                                               (first entry)
90 AAWDDSLSEFL 100
                                                                                                                                                                                                                                              Main SH,
                                                                                                                                                                                                                                                              WPI; 2001-282031/29.
                                                                                                                                                                                                                                                                      N-PSDB; AAS03512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110 AA;
                                                                                                                                                          WO200127279-A1
                                                                                                                                                                                                             12-OCT-1999;
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                              Edwards BM,
                                                                               29-AUG-2001
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                                                                                                                                                                                                                                                                                                         diseases
                                                               AAU02612;
                               RESULT 6
                                        AAU02612
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
condition. The antibodies can be used in the treatment of obesity and
cobesity related diseases. The antibodies can be used to deliver drugs or
con be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
configuration of the surface of an adipocyte colle
consed in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.

Constituted the consence of level of adipocytes in a cell or tissue sample.

Constituted the than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
constituted and the heart disease
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                                       Gaps
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100.0%; Score 58; DB 4; Length 110;
100.0%; Pred. No. 0.024;
ive 0; Mismatches 0; Indels
     Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                            1 AAWDDSLSEFL 11
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AAWDDSLSEFL 100
    90
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AAU02627 standard; protein; 110 AA.
AAU02627
ID AAU0
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Antibody; adipocyte; heavy chain; light chain; obesity; fat;

Anti-adipocyte monoclonal antibody light chain, FAT 113.

(first entry)

29-AUG-2001

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AAU02629;

AAU02629 standard; protein; 110 AA

RESULT 8 AAU02629

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consistences of anti-adipocyte monoclonal antibody heavy chain, light chain, and neavy chain complementarity determining regions (CDR) of the and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and cobsity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to can be used as a therapeutic itself. Antibodies binding specifically to can be used as radiolabel, fluorescent or chemical group and detectable label such as radiolabel, fluorescent or chemical group and cused in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related Gaps and AAU02641-AAU02748 represent the amino acid ö fat; 100.0%; Score 58; DB 4; Length 110; 100.0%; Pred. No. 0.024; ive 0; Mismatches 0; Indels Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR. nti-adipocyte monoclonal antibody light chain, FAT 112. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. Claim 1; Page 172; 182pp; English. 11-OCT-2000; 2000WO-GB003900. 99US-0158812P 29-AUG-2001 (first entry) Local Similarity hes 11; Conservative Edwards BM, Main SH, WPI; 2001-282031/29. AAU02501-AAU02635, N-PSDB; AAS03527 Sequence 110 AA; WO200127279-A1 Homo sapiens. .2-OCT-1999; 19-APR-2001. Query Match diseases. Matches

heart disease; complementarity determining region; CDR 11-OCT-2000; 2000WO-GB003900 WO200127279-A1 Homo sapiens. 19-APR-2001

99US-0158812P 12-OCT-1999; (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Vaughan TJ; Edwards BM, Main SH,

WPI; 2001-282031/29. N-PSDB; AAS03529.

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related дівеавев.

Claim 1; Page 173; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
closeity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
be complement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies binding specifically to
by complement mediated lysis. The antibodies by the determine the
closed in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposites can also be produced e.g. intraabdominal fat associated with heart disease

Sequence 110 AA;

Gaps ö Query Match 100.0%; Score 58; DB 4; Length 110; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 11; Conservative 0; Mismatches 0; Indels

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RESULT 9

AAW19883 standard; protein; 111 AA AAW19883; AAW19883 THERESEANCE

07-DEC-1997 (first entry)

CEA-specific antibody CEA1, CEA2, CEA3 VL sequence

Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.

Homo sapiens

Location/Qualifiers Key Region

23. .35
/label= CDR1
/note= "complementarity determining region 1"

Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer. This polypeptide sequence comprises the light chain variable region (VL) of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2 and CEA3. VH (AAT72126-13) and VL (AAT7213-15) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see AAM)8976-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-83 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7, or their CDR sequences, as well as CEA6 VH and VL variants. (A) is used to detect cells expressing cancer, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast 50. .56
/label= CDR2
/note= "complementarity determining region 2"
/note= "complementarity determining region 3"
/label= CDR3
/note= "complementarity determining region 3" CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. Mccafferty JG; Claim 14; Fig 1b; 128pp; English. 95GB-00025004. 96WO-GB003043 96GB-00010824 96GB-00021295 Osbourn JK, Allen DJ, WPI; 1997-319779/29. N-PSDB; AAT72133 Sequence 111 AA; WO9720932-A1 09-DEC-1996; 11-OCT-1996; 07-DEC-1995; 12-JUN-1997. Region Region

Gaps ö 100.0%; Score 58; DB 2; Length 111; 100.0%; Pred. No. 0.025; 1. Indels 1. Mismatches 0; Indels Query Match
Best Local Similarity 100.

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AAU02542 standard; protein; 111 AA. AAU02542; RESULT 10 AAU02542

Anti-adipocyte monoclonal antibody light chain, FAT 30

(first entry)

29-AUG-2001

fat; Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.

Ношо варіенв

WO200127279-A1

19-APR-2001.

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Sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies binding specifically to adipocyte can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese content types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
                                                                                                                                                                                                                                                                                                                                                                                                     Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 118-119; 182pp; English.
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                                                                                                                                                                                                                                        Vaughan TJ
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                                11-OCT-2000; 2000WO-GB003900.
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                                                                                                                                                                                                                                        Main SH,
                                                                                                                                                                                                                                                                                                        WPI; 2001-282031/29.
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Main SH,

Edwards BM,

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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
cinvention. The antibodies can be used in the treatment of obesity and
cinvention. The antibodies can be used to deliver drugs or
pro-trugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
considered the mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
considered antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
considered than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposite can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                                             Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
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                                                                                                                                        Claim 1; Page 124; 182pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                2001-282031/29
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                                 N-PSDB; AAS03451
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
twention. The antibodies can be used in the treatment of obesity and
consists a constant of the far mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
can be used as a therapeutic itself. Antibodies binding specifically to
can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
catipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies binding specifically to
catipocytes and as radiolabel, fluorescent or chemical group and
catectable label such as radiolabel, fluorescent or chemical group and
cused in methods of diagnosis in human subjects e.g. to determine the
catectable label such as radiolabel, fluorescent or chemical group and
catectable the presence or level of adipocytes in a cell or tissue sample.

The antibodies can be used as an alternative means of traatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
con different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease
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                                Claim 1; Page 146; 182pp; English
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Matches 11; Conservative
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N-PSDB; AAS03506.
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AAU02606
AC AAU02
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can be used as a therapeutic itself. Antibodies binding specifically to adjocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adjocyte antigen on the surface of an adjocyte to detect or determine the presence or level of adjocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients of the unundergoing surgery to remove axcess fat. Antibodies abdominal fat associated with heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG34301 standard; protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurokinin B antibody SEQ ID NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2003; 2003WO-US016802.
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                                                                                                                                                                                                                                                           Local Similarity 100
                                                                                                                                                                                                                                                                                                                                   91 AAWDDSLSEFL 101
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N-PSDB; ADG34282.
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                                                                                                                                                                                                             Sequence 111 AA;
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New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
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                                                                              ADG34317 standard; protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                     Neurokinin B antibody SEQ ID NO:40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2003; 2003WO-US016802.
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N-PSDB; ADG34298.
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RESULT 15
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The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or preclampsia. The present sequence is used in the exemplification of the invention. Ouery Match 100.0%; Score 58; DB 8; Length 242; Best Local Similarity 100.0%; Pred. No. 0.056; Matches 11; Conservative 0; Mismatches 0; Indel8 Sequence 242 AA;

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Search completed: October 14, 2005, 16:12:42 Job time : 84.5625 secs g

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Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 374, App Sequence 346, App Sequence 346, Appl Sequence 60, Appl Sequence 497, App Sequence 41, App Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 11, App Sequence 11, App Sequence 6, Appl Sequence 6, Appl Sequence 11, App Sequence 13, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 36, Appl Sequence 43, Appl Sequence 39, Appl Se
                                                                                                                                                                                                               ; Search time 21.6562 Seconds (without alignments) 37.917 Million cell updates/sec
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-273-146-63
US-08-252-816A-15
US-08-350-260A-374
US-09-104-337A-346
US-09-104-337A-346
US-09-104-337A-497
US-09-240-274-59
US-08-665-202-36
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US-08-665-202-374-36
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Maximum Match 100%
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Sequence 19, Appl Sequence 112, Appl Sequence 113, Appl Sequence 5, Appl Sequence 5, Appl Sequence 4, Appl Sequence 4, Appl Sequence 7, Appl Sequence 7, Appl Sequence 10, Appl Sequence 146,	11 e s	Length 11; Indels 0; Gaps 0;
US-09-315-574-39 US-08-211-202-112 US-08-211-202-113 US-08-665-202-5 US-09-315-574-5 US-09-315-574-5 US-09-956-086-4 US-09-956-087-4 US-09-956-087-4 US-09-985-427-7 US-09-985-427-7 US-09-985-427-7 US-09-983-880-7 US-09-315-574-40 US-09-315-574-40 US-08-350-260A-446 US-08-350-260A-446 US-08-350-260A-446 US-08-350-260A-446	ALIGNMENTS IS-09-383-667-15 Sequence 15, Application US/09383667 Sequence 15, Application US/09383667 Batent No. 6624295 GENERAL INFORMATION: APPLICANT: Adams, Camelia W. APPLICANT: Baton, Dan L. APPLICANT: Baton, Dan L. APPLICANT: Hass, Philip E. APPLICANT: Kirchhofer, Daniel APPLICANT: Kirchhofer, Daniel APPLICANT: Kirchhofer, Daniel APPLICANT: Wichhofer, Daniel APPLICANT: Wichhofer, Daniel APPLICANT: Wichhofer, Daniel APPLICANT: Human Anti-Factor IX/IXa Antibodies FILE OF INVENTION: Human Anti-Factor IX/IXa Antibodies FILE REFERENCE: P1661R2 CURRENT FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-08-26 EARLIER FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 32 ELENGTH: HI TYPER: PRT ORGANISM: Homo sapiens	re 58; DB 4; 1. No. 0.00037; Ismatches 0;
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44444444444444444444444444444444444444	ALL SULT 1 -09-383-667-15 Sequence 15, Application US/09383667 Betent No. 6624295 GENERAL INFORMATION: APPLICANT: Adams, Camelia W. APPLICANT: Eaton, Dan L. APPLICANT: Eaton, Dan L. APPLICANT: Eaton, Dan L. APPLICANT: Suggett, Shalley TITLE OF INVENTION: Human Anti-Fact. FILE REFERENCE: P16612- CURRENT APPLICATION NUMBER: US/09/3 CURRENT APPLICATION NUMBER: US 60/0 EARLIER FILING DATE: 1999-08-26 EARLIER PILING DATE: 1999-08-26 EARLIER PILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 32 LENGTH: 11 TYPE: PT	harity Conservat AAWDDSLSEFL AAWDDSLSEFL AAWDDSLSEFL AAWDDSLSEFL S-63 S-63 S-63 WFORMATION WT: Smith, Ro WT: Smith, Ro WT: Taltmas, R WT: Higgeral WT: Renen, J WT: Fitzgeral WT: Martin, M WT: Martin, M WT: Taltmas, R WT: Taltmas, R
	1 1 -383-667-15 -383-667-15 ent no. 6624 ERAL INFORMAY PLICANT: Adar PLICANT: Baty PLICANT: DEVLICANT: Baty PLICANT: Adar PLICANT: Adar PLICANT: Adar PLICANT: Sug PLICANT: Sug PLICANT: Sug REENT APPLICY RRENT APPLICY RRENT APPLICY RRIER FILING RRIER FI	latch 11; 146-63 and 146-63 and 158-63 and 168-63 and 1
00000000000000000000000000000000000000	RESULT 1 US-09-383-667-15 Sequence 15, Application US/0936 Parent No. 6624295 GENERAL INFORMATION: APPLICANT: Adms, Camelia W. APPLICANT: Devaux, Brigitte APPLICANT: Baton, Dan L. APPLICANT: Uddice, J. Kevin APPLICANT: Lass, Philip E. APPLICANT: Uddice, J. Kevin APPLICANT: Willip E. APPLICANT: UNGREV. Daniel APPLICANT: Shelley TILE REPERENCE: P1661R2 CURRENT APPLICATION NUMBER: US CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 1998-08-28 EARLIER FILING DATE: 1998-08-28 EARLIER PPLICATION NUMBER: US EARLIER FILING DATE: 1998-08-28 EARLIER PLING DATE: 1998-03-03 SEQ ID NO 15 LENGTH: 11 TYPE: PRT CORGANISM: Homo sapiens	Query Match Best Local Similarity 100.0%; Pred Matches 11; Conservative 0; M. Oy 1 AAWDDSLSEFL 11 Db 1 AAWDDSLSEFL 11

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PILING DATE: 02-DEC-1991

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206372.6

FILING DATE: 23-SEP-1992

PRIOR APPLICATION DATA:

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PRIOR APPLICATION DATA:

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/244,597

FILING DATE: 01-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: DAVIG W. CIOUGH

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/33308

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 374, Application US/08350260A Patent No. 5962255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i: 111 amino acids
amino acid
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Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AAWDDSLSEFL 100
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60606-6402
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               TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 Bast Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Patent No. 5872215
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
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CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
PILING DATE: 23-MAY-1996
PRIOR APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: US/08/273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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amino acid
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAWDDSLSEFL 11
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US-08-652-816A-15
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Gaps
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APPLICANT: Williams, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Waster, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Dinding pairs
NUMBER OF SEQUENCES: 602
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100.0%; Score 58; DB 2; Length 111; 100.0%; Pred. No. 0.0044; Pred. No. 0. 10044; ive 0; Mismatches 0; Indel8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FLING DATE: 05-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: Marshall, O'Toole, Gerstein, Macker Drive
CITY: Chicago
STRYE: Chicago
COUNTRY: USA
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APPLICANT: Winter, Gregory Paul
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Williams, Samuel Cameron
APPLICANT: Wilsim, Abuva
APPLICANT: Nissim, Abuva
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: Dinding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: Marshall, O'Toole, Gerstein, Macker Drive
CITY: Chicago
STATE: Illinois
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
                                              FILING DATE: 25-Jun-1998
PRIOR APPLICATION NUMBER: US 08/350,260
FILING DATE: 25-Jun-1994
APPLICATION NUMBER: US 08/350,260
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/30,619
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/30,619
FILING DATE: 15-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BARTICON NUMBER: 28111/32372A
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                               APPLICATION NUMBER: US/09/104,337A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQ ID NO: 374: US-09-104-337A-374
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; Patent No. 5962255
; GENERAL INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.3
Best Local Similarity 72.7
Matches 8; Conservative
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Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSES: Audrey L. Bartnicki
STREET: Marehall, Geretein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.3%; Score 46; DB 2; Length 11; 72.7%; Pred. No. 0.05;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 34-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 38,107
REFERENCE/DOCKET NUMBER: 374:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nissim, Ahuva
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COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.3
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAWDDSLSEFL 11
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US-08-350-260A-374
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Gaps

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Sequence 60, Application US/08665202

Sequence 60, Application US/08665202

Batent No. 597322

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC Compatible
COMPUTER: Floppy disk
COMPUTER: THE PC Compatible
COMPUTER: THE PC COMPUTER:
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGEN INFORMATION:
NAME: Bartnickt, Audrey L.
REGISTRATION NUMBER: 40,499
REFRENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-690
INFORMATION FOR SEQ ID NO: 346:
             PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 13-MAX-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
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SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-09-104-337A-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 11 amino acids
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Best Local Similarity 72.7
Matches 8; Conservative
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ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-665-202-60
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Nissim, Ahuva
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 11; Pred. No. 0.11;
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                                       APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 34-MAR-1993
PRIOR APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
ATTORNEY/ASERY INFORMATION:
APPLICATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 
TELECOMMUNICATION INFORMATION:
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Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
HUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.9%;
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LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Patent No. 6512097

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Pour Embarcadero Center, Suite 1100

CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1996
ATPONEY/AGERT INFORMATION:
AMADE: ALLOCATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION POR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02307E-061411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 9 amino acids
                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: '
SEQUENCE CHARACTERISTICS:
                                                                          LENGTH: 10 amino acids
                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
                                                                                                                                           ; TOPOLOGY: linear
US-08-350-260A-497
                                                                                                                                                                                                                                                                                                               1 AAWDDSLS 8
                                                                                              TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Winter, Gregory Paul
APPLICANT: Wilfiths, Andrew David
APPLICANT: Wilfiams, Samuel Cameron
APPLICANT: Wilfiams, Samuel Cameron
APPLICANT: Wissim, Ahuva
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.25 (EPO)

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/350,260A

FLING DATE: 05-DEC-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: GB 9110549.4

FILING DATE: 15-MAX-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB91/01134

FILING DATE: 10-JUL-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAX-1993

RROR APPLICATION DATA:

FILING DATE: 24-MAX-1993

RROR APPLICATION DATA:

FILING DATE: 24-MAX-1993

RROR APPLICATION DATA:

FILING DATE: 31-MAX-1994

RROR APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAX-1994

RROR APPLICATION NUMBER: US 08/307,619
                                                                                                                                                Length 10
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                                                                                                                                                  74.1%; Score 43; DB 2; 100.0%; Pred. No. 0.15;
                                                                                                                                                                                                  0; Mismatches
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REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 497, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
         LENGTH: 10 amino acids
                                                                                                                                                Query Match 74.1
Best Local Similarity 100.
Matches 8; Conservative
                             ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY:
US-08-350-260A-339
                                                                                                                                                                                                                                                                            1 AAWDDSLS 8
                                                                                                                                                                                                                                                 1 AAWDDSLS 8
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STATE: Illinois
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| SEGURATION RES REQ ID NO: 497:
| SEGURATION RES REQ ID NO: 497:
| LENGTH: 10 anino scide
| CTRANDERSES: eiler | Anino scide
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| SEGURATION: | Anino scide | Anino scide |
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; SEQUENCE DESCRIPTION: SEQ ID NO: 497; US-09-104-337A-497
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US-09-104-337A-497
Sequence 497, Application US/09104337A
Fatent No. 6492160
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nassim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
Smith, Andrew John Hammond
Johnson Kevin Stuart
Smith, Andrew John Hammond
Johnson Merion John Hammond
Johnson Merion John Hammond
Johnson Merion John Hammond
Johnson Merion John Hammond
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STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EDOPY disk
COMP
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                                                                                                                                                                                                                                   74.1%; Score 43; DB 4; Length 10; 100.0%; Pred. No. 0.15; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSES Audrey L. Bartnicki
STREET: Marehall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 497:
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 339:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                               Query Match
Best Local Similarity 100...
8; Conservative
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US-09-104-337A-339
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; Sequence 441 Application US/08350260A
; Patent No. 5862555
; GENERAL INFORMATION:
    APPLICANT: Winter, Gregory Paul
    APPLICANT: Williams, Samuel Cameron
    APPLICANT: Williams, Samuel Cameron
    APPLICANT: Williams, Samuel Cameron
    APPLICANT: Waterhouse, Peter
    APPLICANT: Waterhouse, Peter
    APPLICANT: Smith, Ahuva
    APPLICANT: Smith, Andrew John Hammond
    TITLE OF INVENTION: Methods for producing members of specific
    TITLE OF INVENTION: Dinding pairs
    NUMBER OF SEQUENCES: 602
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: David W. Clough
    STREET: Marshall, O'Toole, Gerstein, Murray & Borun
    STREET: 6300 Sears Tower, 233 South Wacker Drive
    CITY: Chicago
    STAPE: Illinis
    COUNTRY: USA
    ZIP: KARAC
     74.1%; Score 43; DB 4; Length 10; 100.0%; Pred. No. 0.15; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 606.6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GF 9206318.9
FILING DATE: 10-UL-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-UL-1991
PRIOR APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 15-MAY-1992
PRIOR APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION NUMBER: US 08/307,619
FILING DATE: 31-MAR-1994
PRIOR APPLICATION NUMBER: US 08/307,619
FILING DATE: 31-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Clough, David W
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                   1 AAWDDSLS
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Job time : 21.6562 secs

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Sequence 6, Application US/08665202
Sequence Context Nation No. 5977322
TITLE OF INVENTION: No. 59773221 High Affinity Human Antibodies to TITLE OF INVENTION: No. 597732221 High Affinity Human Antibodies to TITLE OF INVENTION: Uncortained and Townsend and Crew LLP Context OF Sequence Context Conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                       Query Match

74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLCGY: linear
US-08-350-260A-441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                  1 AAWDDSLS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAWDDSLS
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US-08-665-202-6
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Search completed: October 14, 2005, 16:22:03

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October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds (without alignments) 58.615 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Sequence 40, Appl Sequence 1927, Ap Sequence 29, Appl Sequence 33, Appl Sequence 36, Appl Sequence 1926, Ap Sequence 1926, Ap Sequence 1926, Ap Sequence 24, Appl Sequence 40, Appl US-10-981-692-24 US-10-981-622-40 US-09-880-748-1927 US-10-293-418-1927 US-10-981-632-29 US-10-981-632-26 US-10-981-622-26 US-10-291-622-26 US-10-291-622-26 US-10-293-418-1926 US-10-293-418-1926 US-10-293-418-1926 US-10-293-418-1926 100.0 100.0 100.0 100.0 100.0 100.0 100.0 3 7 110 110

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ALIGNMENTS

ö RESULT 1

US-10-981-692-24

i Sequence 24, Application US/10981692

i Sequence 24, Application US/10981692

i Sequence 24, Application US/10981692

i GENERAL INFORMATION:

i APPLICANT: Rosen et al.

i TITLE OF INVENTION: Annibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PF590P1

CURRENT PELING DATE: 2004-11-05

PRIOR APPLICATION NUMBER: PCT/US03/16802

PRIOR APPLICATION NUMBER: PCT/US03/16802

PRIOR APPLICATION NUMBER: 60/383,802

PRIOR APLICATION NUMBER: 60/383,802

PRIOR FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SEQ ID NO 24

LENGTH: 242 Gaps ö 100.0%; Score 58; DB 18; Length 242; 100.0%; Pred. No. 0.048; Live 0; Mismatches 0; Indels ; FEATURE: ; OTHER INFORMATION: NO15E08 SCFV US-10-981-692-24 TYPE: PRT ORGANISM: Artificial sequence Best Local Similarity 100 Matches 11; Conservative 221 AAWDDSLSEFL 231 1 AAWDDSLSEFL 11 Query Match g ઠે

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AFPLICANT: RUBEN et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PELICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: 60/340,817
PRIOR PELICATION NUMBER: 60/294,499
PRIOR PELICATION NUMBER: 60/293,499
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PELING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2000-10-17
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US-10-981-692-29
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ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-293-418-1927
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US-10-981-692-29
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US-10-981-692-40

Sequence 40, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

FILE REFERENCE: PF590P1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT PRILING DATE: 2004-11-05

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 40

LEASTH: 242
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Sequence 1927, Application US/0980748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF533

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

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ORGANISM: Artificial sequence
FEATURE:
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-880-748-1927
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Sequence 29, Publication No. US20050163777A1
HINDORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1
CURRENT FILING DATE: 2004-11-05;
PRIOR APPLICATION NUMBER: US/10/981,692;
PRIOR APPLICATION NUMBER: PCT/US03/16802;
PRIOR APPLICATION NUMBER: 60/383,802;
PRIOR PILING DATE: 2002-05-30;
PRIOR PILING DATE: 2002-05-30;
PRIOR PILING DATE: 2002-05-30;
NUMBER OF SEQ ID NOS: 76;
SOFTWARE: PatentIn version 3.1;
LENGTH 243
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100.0%; Score 58; DB 15; Length 243; 100.0%; Pred. No. 0.048; ive 0; Mismatches 0; Indels 0
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US-10-981-692-33
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US-10-293-418-1927 ; Sequence 1927, Application US/10293418 ; Publication No. US20030223996A1

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                                                  APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B FILE REFERENCE: PF590P1

CURRENT APPLICATION NUMBER: US/10/981,692

CURRENT PAPLICATION NUMBER: US/10/981,692

CURRENT PAPLICATION NUMBER: PCT/US03/16802

PRIOR APPLICATION NUMBER: PCT/US03/16802

PRIOR PILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: 60/383,802

PRIOR FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1

LENGTH: 243
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
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Sequence 33, Application US/10981692
Publication No. US20050163777A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: N023E01 BCFv
US-10-981-692-33
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US-10-981-692-26
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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US-09-880-748-1926
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Sequence 1926, Application US/10293418

Publication No. US20030223996A1

Sequence 1926, Application US/10293418

Publication No. US20030223996A1

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PLICATION NUMBER: 60/340,817

PRIOR PLICATION NUMBER: 60/340,817

PRIOR PLILING DATE: 2001-12-19

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-03-16

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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VET: 2.0
LENGTH: 245
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; Sequence 3241, Application US/10293418
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Best Local Similarity 100.
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; ORGANISM: Homo sapiens
US-09-880-748-1926
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; ORGANISM: Homo sapiens
US-10-293-418-1926
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JOS-09-80-140-141-14

Sequence 1913, Application US/0980748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICAMTION:

APPLICAMTION: Antibodies that Immunospecifically Bind BLyS

FILE REFRENCE: PF53

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 2329

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1913

LENGTH: 246

TYPE: PRI

CORDANISM: Homo sapiens

US-09-880-748-1913
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; ORGANISM: Homo sapiens
US-09-880-748-1917
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Best Local Similarity
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Sequence 31, Application US/10981692

Publication No. US20050163777A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
FILE REPERENCE: PFS90P1

CURRENT PFLING DATE: 2004-11-05

PRIOR PILING DATE: 2004-11-05

PRIOR PLING DATE: 2003-05-29

PRIOR PLING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE PLING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 76

SEQ ID NO 31

LENGTH: 245
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                                   GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-11-16

PRIOR PELING DATE: 2001-12-19

PRIOR PELING DATE: 2001-12-19

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PELING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/210,016

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-01-17

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

LENGTH: 245

TURNGETH: 245
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Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial sequence FEATURE:
Publication No. US20030223996A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-293-418-3241
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US-09-880-748-1917

| Sequence 1917, Application US/0980748|
| Publication No. US20030059937A1|
| GENERAL INFORMATION:
| TITLE CANT: Ruben et al. |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION NUMBER: 60/212,210 |
| PRIOR PILING DATE: 2000-06-15 |
| PRIOR PILING DATE: 2000-06-15 |
| PRIOR PILING DATE: 2001-03-16 |
| PRIOR PILING DATE: 2001-03-16 |
| PRIOR PILING DATE: 2001-03-21 |
| PRIOR PILING DATE: 2001-03-25 |
| NUMBER OF SEQ ID NOS: 3239 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 1917 |
| LENGTH: 246 |
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RESULT 12

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**RESULT 14
US-10-293-418-1913

**SEQUENCE 1913, Application US/10293418

**SEQUENCE 1913, Application US/10293418

**Publication No. US20030223996A1

**GEMERAL INFORMATION:

**APPLICANT: Ruben et al.

**TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

**FILE REFERENCE: PF523P2

**CURRENT PILING DATE: 2002-11-27

**PRIOR APPLICATION NUMBER: 09/310,817

**PRIOR PILING DATE: 2001-11-16

**PRIOR PILING DATE: 2001-12-19

**PRIOR PILING DATE: 2001-06-15

**PRIOR PILING DATE: 2001-06-15

**PRIOR PILING DATE: 2001-06-25

**PRIOR PILING DATE: 2001-03-16

**PRIOR PILING DATE: 2001-01-17

**PRIOR PILING DATE: 2000-06-16

**PRIOR PILING DATE: 200
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US-10-293-418-1917

i Sequence 1917, Application US/10293418

i Publication No. US20030223996A1

i GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibone te al.

TITLE OF INVENTION: Antibone te al.

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 00/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-25

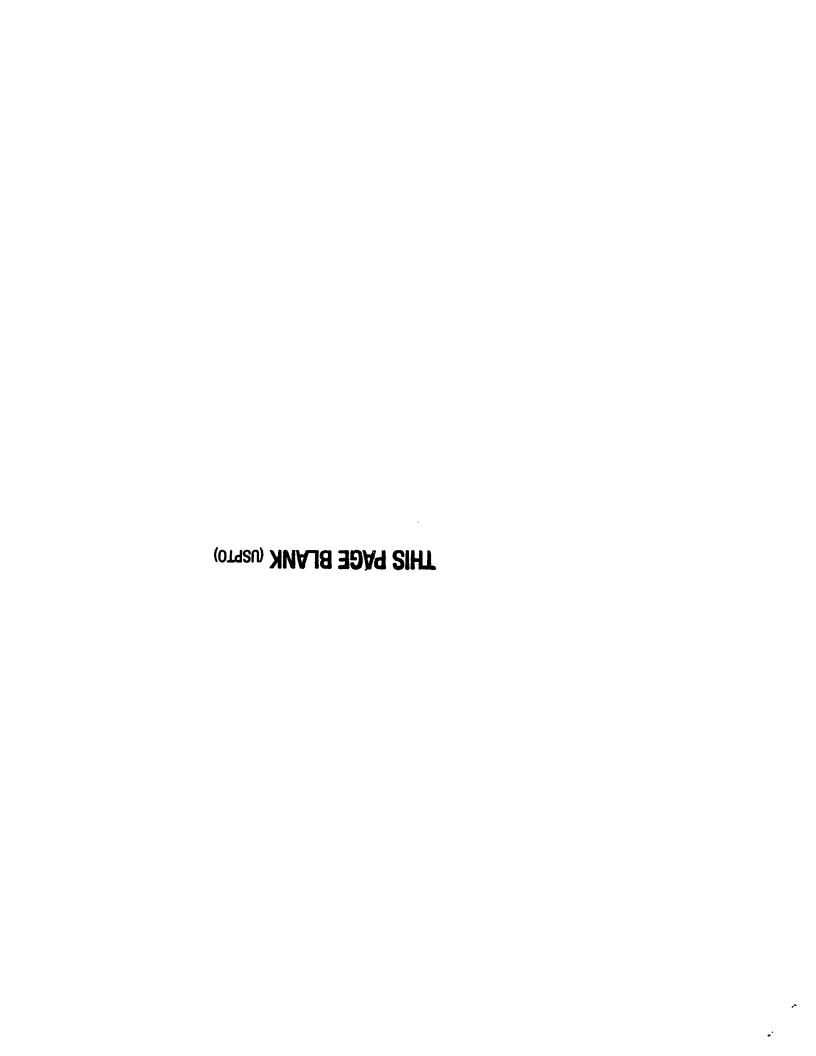
PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1977
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Best Local Similarity 100.
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-293-418-1913
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                             Query Match
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels (
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                                                                                                                      225 AAWDDSLSEFL 235
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US-10-293-418-1917
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using sw model OM protein - protein search,

October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds (without alignments) 69.190 Million cell updates/sec Run on:

US-10-614-959-15 58 Title: Perfect score: Sequence:

1 AAWDDSLSEFL 11

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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æ	Query Match	74.1	74.1	74.1	70.7		σ	69.0	e.	69.0	69.0	69.0	69.0	69.0	69.0	69.0	0.69	69.0	67.2	67.2	67.2	67.2	~	_	65.5	S	S	65.5	'n	S.
	Score	43	43	43	41	40	40	40	40	40	40	40	40	40	40	40	40	40			39									
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166	259	371	305	,	476	644	655	857	1485	184	184	184	184	227	280	280
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37.5	37	37	3.7	. (3.7	37	37	37	37	36	36	36	36	36	36	36
30	31	32	33	;	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

S36048 To lambda chain - human (fragment) C;Species: Howo sapiens (man) C;Species: Howo sapiens (man) C;Species: Howo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 C;Accession: S36048; S36049 R;Williams, S.C. Submitted to the EMBL Data Library, April 1993 A;Reference number: S36046 A;Reference number: S36046 A;Reference number: DNA A;Residues: prellminary A;Residues: L-98 - WILL> A;Residues: L-98 - WILL> A;Residues: L-98 - WILL> A;Cross-references: EMBL:222189; NID:G312294; PIDN:CAA80199.1; PID:G312295; EMBL:222190 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin homology	EMBL: 222190	
in - human (fragment) mo saplens (man) v-1993 #sequence_revision 01-Dec-15 S36048; S36049 the EMBL Data Library, April 1993 unber: S36046 11minary pe: DNA pe: DNA pe: DNA i immunoglobulin V region; immunoglobulin s: immunoglobulin	.DN:CAA80199.1; PID:g312295; .obulin homology	995 #text_change 21-Jan-2000
1g landda chain - hum 1g landda	A;Residues: 1-98 <wil.> A;Cross-references: EMBL:Z22189; NID:g312294; PI C;Superfamily: immunoglobulin V region; immunogl C;Keywords: heterotetramer; immunoglobulin F;15-91/Domain: immunoglobulin homology <imm.></imm.></wil.>	\$36048 Ig lambda chain - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 01-Dec-19 C;Accession: 836048; 836049 R;Williams, S.C. R;Williams, S.C. Submitted to the BMBL Data Library, April 1993 A;Reference number: 836046

ö Query Match 74.1%; Score 43; DB 2; Length 98; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 8; Conservative 0; Mismatches 0; Indels

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Gaps

90 AAWDDSLS 97

1 AAWDDSLS 8

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RESULT 2
S78058
Granda chain precursor V-J region (clone mAB 67VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78058; S23723
R;Harindranath, N...

submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78058

A; Molecule type: mRNA
A; Residues: 1-129 < HAR>
A; Residues: 1-129 < HAR>
A; Cross-references: EMBL:X5446; NID:g37923; PIDN:CAA38313.1; PID:g930121
A; Cross-references: EMBL:X5446; NID:g37923; PIDN:CAA38313.1; PID:g930121
B; Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins, Int. Immunol. 3, 865-875, 1991
A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hi

A, Reference number: S23716; MUID: 92031262; PMID: 1718404

A;Accession: S23723
A;Molecule type: mRNA
A;Residues: 19-129 «HAM»
A;Cross-references: EMBL:X54446
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin (fragment) #status predicted <SIG>F;1-18/Domain: signal sequence (fragment)

Best Local Similarity 100. Matches 8; Conservative

Query Match

108 AAWDDSLS 115

Ig lambda chain - human

1 AAWDDSLS 8

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C;Accession: 849571

C;Accession: 849571

R;Giachino, C.; Padovan, E.; Lanzavecchia, A.

Rubmitted to the EMBL Data Library, November 1994

A;Description: k+1+ dual receptor B cells are present in the human peripheral repertoire.

A;Reference number: 849571
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Ig lambda chain - human (fragment)

Ig lambda chain - human (fragment)

Ig lambda chain - human (fragment)

C;Species: Homo sapiens (man)

C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S36046

B;Williams, S.C.

B;Williams, S.C.

B;Williams, S.C.

B;Reference number: S36046

B;Accession: S36046

B;Accession: S36046

B;Accession: I-98 *WIL>

B;Accession: I-98 *WIL>

B;Coss-references: EWBL: Z22187; NID: G312312; PIDN: CAA80197.1; PID: G312313

C;Superfamily: immunoglobulin V region; immunoglobulin homology
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C'Species: Homo sapiens (man)
C'Species: How-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C'Accession: S36047
R.Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A,Reference number: S36046
A,Reference number: S36047
A,Accession: S36047
A,Accession: S36047
A,Residues: preliminary
A,Molecule type: DNA
A,Residues: 1-98 «WIL-
A,Cross-references: EMBL:Z22188; NID:G312291; PIDN:CAA80198.1; PID:G312292
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer: immunoglobulin
F;15-91/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                    Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S49571
A;Status: preliminary
A;Molecule type: mRNA
A;Residus: 1-95 GMBL:Z46625; NID:g575259; PIDN:CAA86595.1; PID:g575260
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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87.5%; Pred. No. 4.4;
tive 1; Mismatchee
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Pred. No. 4.2;
1; Mismatches
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Best Local Similarity 87.5
Matches 7; Conservative
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91 AAWDDSLDGYV 101
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76 AAWDDSLT 83
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Best Local Similarity
Matches 7; Conserv
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A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;IS-92/Domain: immunoglobulin homology <IMM>
F;IF-92/Domain: immunoglobulin homology <IMM>
F;IF-92/Domain: shandifide sarboxylic acid (Gln) #status experimental
F;22-90/Disulfide bonds: #status predicted
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R,Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
Bur. J. Biochem. 150, 349-357, 1985
A;Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem A;Reference number: A25479; MUID:85257662; PMID:2410269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: 822750
R;Combristo, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: 82550
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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A;Note: residues 33-36 and some of the sequenced peptides were positioned by homology
C;Comment: The C region of this chain has the Mcg+ and Kern+ markers.
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                    Gaps
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         F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>F;33-109/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.4;
2; Mismatches 2; Indels
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100.0%; Pred. No. 3.3;
ative 0; Mismatches
                                                                                                         DB 2;
                                                                                                     74.1%; Score 43; DB 100.0%; Pred. No. 1.7 tive 0; Mismatches
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Ig lambda chain V-I region (Mem) - human

A; Molecule type: protein A; Residues: 1-112 <MIH>

C; Genetics:

Query Match Best Local Similarity 100..

A; Residues: 1-235 < COM>

109 AAWDDSLS 116

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1 AAWDDSLS 8

70.7%; 63.6%;

Query Match
Best Local Similarity 63.6
Matches 7; Conservative

1 AAWDDSLSEFL 11

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C; Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative

ઠે g A; Cross-references: UNIPROT: P04208

A;Molecule type: protein A;Residues: 1-109 <TAK>

5 I6:39:24 2005

Mon Dec

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Signoid and a chain V region - human (fragment)
C) Species: Homo sapiens (man)
C) Species: Homo sapiens (man)
C) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C) Accession: 823626
R:Olee, T: Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; (
S. Saperia: Signoid S
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Cispecies: Homo sapiens
Cispecies: Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cispecies: Sispient (manage)
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S2578;
K;Combriato, G; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamba.
A;Reference number: $16439; MUID:91257162; PMID:1904362
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Pred. No. 6.9;
1; Mismatches
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; Pred. No. 11;
1; Mismatches
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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87.5%;
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Best Local Similarity 87.5.
Pest Local 7; Conservative
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Matches 7; Conservative
|||||||:
109 AAWDDSLN 116
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109 AAWDDSLN 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig lambda chain V-I region (Wah) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: O4-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004 C;Accession: A01967 B;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, P.W. R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, P.W. Affitle: Complete covalent structure of a human immunoglobulin D: sequence of the lambda A;Reference number: A01967; MUID:83221661; PMID:6407018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:IGLV@
A;Gene: GDB:IJ9342; OMIM:147240
A;Cross-references: GDB:IJ9342; OMIM:147240
A;Cross-references: GDB:IJ9342; OMIM:147240
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamally: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;1-97/Region: V segment
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: 823627
R;Olee, T.; Lu, B.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from the A;Reference number: 823623; MUID:92156804; PMID:1740665
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A;Molecule type: DNA
A;Residues: 1-117 <OLE>
A;Cross-references: EMBL:X59707; NID:g34426; PIDN:CAA42228.1; PID:g34427
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;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotetramer; immunoglobulin
;34-110/Domain: immunoglobulin homology <IMM>
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                                                                                      Length 98;
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                                                                            Score 40; DB 2;
Pred. No. 4.4;
1; Mismatches
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Pred. No. 4.9;
0; Mismatches
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F:22-89/Disulfide bonds: #status predicted
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69.0%; 80.0%;

8; Conservative

Query Match Best Local Similarity Matches 8; Conserv

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1 AAWDDSLS

A;Residues: 1-234 <COM>

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Search completed: October 14, 2005, 16:23:41 Job time : 16.2969 secs
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R;Combriato, G.; Klobeck, H.G.
R;Combriato,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conserved hypothetical protein CC1169 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87394
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Ci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A67249; MUID:21173698; PMID:11259647
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A;Cross-references: UNIPROT:Q9A925; GB:AE005673; NID:g13422491; PIDN:AAK23153.1; GSPDB:C
C;Genetics
A;Genetics
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C;Spacies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;149-217/Domain: immunoglobulin homology <IMM>
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87.5%; Pred. No. 18;
iive 1; Mismatches
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Matches 7; Conservative
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SAWDDSLS 145
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RESULT 15

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Pred. No. 26;
1; Mismatches
                                                                                                       vuery Match 69.0%;
Best Local Similarity 70.0%;
Matches 7; Conservative 1
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October 14, 2005, 15:51:44; Search time 73.2188 Seconds (without alignments) 76.932 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM protein - protein search, using sw model US-10-614-959-15 58 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 AAWDDSLSEFL 11 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	O968b0 homo sapien	homod				homod	caulc		O9npf8 homo sapien	mus m	O86033 rhizobium m	Q48904 microcystis		_				homo		-	Q74b13 geobacter s	m		_	P45444 emericella	Q73ye0 mycobacteri		031358 brachydanio	-	bacillus	bacillus
		QI .	Q96SB0	QBNEJ1	Q6CLT9	LV1H HUMAN	Q6DHW4	LV1F HUMAN	Q9A925	CEA2_RAT	CEA2_HUMAN	CEA2_MOUSE	GLPK_RHIME	Q48904	YP93_CAEEL	DYHC_NEUCR	Q87GV3	Q6GMV7	KAPI_BOVIN	Q7Z3M1	Q8W0B5	Q6C0Z1	Q74B13	Q7RY83	Q98TR8	YCX7_CHLRE	DYHC EMENI	Q73YE0	Q67NP3	Q31358	Q631V6	Q72Y69	Q815W5
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de	Query	Match	75.9	74.1	74.1	70.7	70.7	69.0	69.0	69.0	σ,	69.0	e.	69.0	69.0	69.0	67.2	67.2	67.2	67.2		67.2	67.2	67.2	67.2	۲.	7	ú	ů.	65.5	ŝ	65.5	65.5
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## ALIGNMENTS

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	SSO NATIONAL MATERIAL	PRELII 00; CC-2001 (TrEM CC-2004 (TrEM R-2004 (TrEM BLreptococca,	ELKALYOCA: Metazoa; Mammalia; Eutheria; MCBI_TAXID=9606; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Adderson E.E., Shikh, "Molecular analysis antibody V region ge J. Immunol. 161:2020 EMBL; U96394; AAB687 FDB; IKU4; Model; L- INTERPRO; IPRO03196; SMART; SM00406; IGV; SMART; SM0406; IGV;	Simi B; AAW      AAW 002 002 004   coal   co

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P06887;
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A Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.P., Jordan H., Moore T., Wang J., Heish F.,
A Hopkins R.P., Jordan H., Moore T., Wang J., Heish F.,
A Hopkins R.P., Jordan H., Moore T., Wang J., Heish F.,
A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
A Hopkins R.P., Jordan H., Porenty M., Rong L.,
A Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Widsin T.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Soderse B.J., Lu X., Gibbs R.A.,
A Holton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
Similar to sployHFC6 Yarrowia lipolytica Calnexin.
ORFNames=KLLA0F00462g; RL 1140.
Bukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetales;
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    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0309984; AAH30984.1; --
HSSP; P01703; 7FAB.
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InterPro; IPR003106; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_wv.
Pfam; PF00564; Cl-set; I.
SWART; SW00406; IGv; 1.
PROSITE; PS00290; IG_LIKE; 2.
Hypothetical protein:
SQUBNCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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100.0%; Pred. No. 11;
tive 0; Mismatches 0
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Best Local Similarity
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Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
"The amino acid sequence of a lambda light chain presenting abnormal physicochemical and antigenic features.";
Eur. J. Blochem. 150:1349-137 (1995).
-!- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides were positioned by homology.
-!- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thlerry A., Wincker C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., "Genome evolution in yeasts.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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PROSITE; PS50835; IG_LIKE; 1.

PROSITE; PS50835; IG_LIKE; 1.

Monoclonal antibody; Pyrrolidone carboxylic acid.

DOMAIN

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Pyrrolidone carboxylic acid.

MOD RES 1 By similarity.
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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EMBL, CR382126; CAG97807.1; ...
InterPro; Prod1540; Calret/Calnex.
InterPro; IPR001898; Calret/Calnex.
InterPro; PR00526; Calret/Callin; 1.
PRINTS; PR00526; Calret/Callin; 1.
PROSTITS; PR001866; Calret/Calnex; 1.
PROSTITS; P800803; CALRETICULIN
PROSTITS; P800803; CALRETICULIN I; 1.
PROSTITS; P800803; CALRETICULIN REPEAT; 1.
SEQUENCE 628 AA; 70981 MW; B0DBA6D1A64644EE CRC64;
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HSSP; P01703; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; 1g: 1.
SMART; SM00406; IGV: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1 lambda chain V-I region MEM.
Homo sapiens (Human).
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tes 6; Conservative
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SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
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Gaps

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/ Match 10.7%; Score 41; DB 1; Length 112; Local Similarity 63.6%; Pred. No. 12; 12; Conservative 2; Mismatches 2; Indels

Best Loc Matches

112 AA; 11789 MW; 748124F079CFFBE4 CRC64;

SEQUENCE Query Match

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C007 %7:60.01 C
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REQUENCE FROM N.A.

RESQUENCE FROM N.A.

REA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Cansavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Foshlyuki S., Carninoi P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Glubs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Glubs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Resyminsh M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human mense only a sequences."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO7843; AAH75643.1; -.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR003599; Ig-1ike.
R InterPro; IPR003599; Ig-1ike.
R InterPro; IPR003597; Ig-1ike.
R InterPro; IPR003596; Ig-MHC.
R InterPro; IPR003596; Ig-MHC.
R EMM: PF00664; Cl-set; I.
Ffam; PF00604; ig-2.
R SMART; SM00409; IG: 2.
R SMART; SM00409; IG: 2.
R SMART; SM00406; IG: 1.
R SMART; SM00406; IG: 1.
R SMART; SM00406; IG: 1.
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R SMART; SM00406; IG: 2.
R SMART; SM00406; IG: 1.
R PROSITE; PS000390; IG: IKE; 2.
R PROSITE; PS000390; IG: MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.7%; Score 41; DB 2; Length 237; 87.5%; Pred, No. 26; 0; Indels rative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                        237 AA
                                                                                                                                                                                                                                                    PRELIMINARY;
                                             91 AAWDDSLDGYV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 87.5
Matches 7; Conservative
1 AAWDDSLSEFL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Q6DHW4
Q6DHW4;
                                                                                                                                                                 RESULT 5

10 066HW4

AC 066HW4

AC 066HW4

DT 25-C

DT 25
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Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Tucomplete covalent structure of a human immunoglobulin D: sequence of the lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.";
The lambda light chain.
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                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%; Score 40; DB 1; Length 109; 80.0%; Pred. No. 18; 1.1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11725 MW; B17785F6A8DF9BAC CRC64;
                                                                                                                                                             20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig lambda chain V-I region WAH.
                                                                                                                                 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J segment.
By similarity.
                                                                                                                               PRT;
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 80.0
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 AAWDDSLWVF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAWDDSLSEF 10
||||||:|
109 AAWDDSMS 116
                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 1
22
109 1
109 AA;
                                                                                                                         LV1F HUMAN P04208;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                  RESULT 6
LV1F HUMAN
                                                                                                                           ò
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SEQUENCE FROM N.A.
STRAINATCC 19089 / CB15;
MEDLINE-21136898; bubmed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE-21136898; bubmed=11259647; DOI=10.1073/pnas.061029298;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Elsen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
KOlonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L., Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter. NCBI_TaxID=155892; 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CC1169.
OrderedLocusNames=CC1169; PRT; PRELIMINARY; Caulobacter crescentus Q9A925 RESULT 7 Q9A925 

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Gaps

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Pfam; PF01412; ArfGap; 1.
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                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., INTERACTION WITH PTDINS(4,5)P2, FTDINS(3,4,5)P3
AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
ARG-275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                           Length 355;
                                                                                                                                                                                                                                                                                                               Indels
                   "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL, AE00595; AAK23153.1; -.
PIR, E87399; TIGR; CC1169; -.
                                                                                                                                        Interpro, IPR011251, Luciferase like.
Pfam; PF00296; Bac luciferase; I.
Complete proteome; Hypothetical protein.
SEQUENCE 355 AA; 38552 MW; 3C4AEF42825E5567 CRC64;
                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                           Score 40; DB 2;
Pred. No. 63;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-0cT-2004 (Rel. 45, Created)
25-0cT-2004 (Rel. 45, Last sequence update)
25-0cT-2004 (Rel. 45, Last annotation update)
Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and lung.
--- SIMILARITY: Contains 1 Arf-GAP domain.
--- SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001849; PH. Threspro; IPR011036; PH related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001164; hRIP like.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ238993; CAB88403.1; -. RGD; 708487; LOC56826.
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         138 SAWDDSLS 145
                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                               1 AAWDDSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Adipocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Centa2;
         Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEA2 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179; Jenne D.E., Tinschert S., Stegmann E., Reimann H., Nurnberg P., Horn D., Naumann I., Buske A., Thiel G.; Acommon set of at least 11 functional genes is lost in the majority of NF1 patients with gross deletions."; Genomics 66:93-97(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=22012451; PubMed=12018390;
Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
Prestwich G.D., Holman G.D.;
"Identification of centarin-alpha2: a phosphatidylinositide-binding
protein present in fat, heart and skeletal muscle.";
Eur. J. Cell Biol. 81:222-230(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                       R->C: Almost complete loss of InsP4 binding.
R->C: Oloss of InsP4 binding. Almost complete loss of InsP4 binding; when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOmo papiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                  GTPage activation; Metal-binding; Repeat; Zinc; Zinc-finger. DOMAIN 9 130 Arf-CAP.
ZN FING 25 48 C4-type.
DOMAIN 131 232 PH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 1; Length 376;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
Bertsch U., Illies C., Mayr G.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 AA; 43524 MW; B357392F38F07166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-COT-2004 (Rel. 45, Last annotation update)
Centaurin alpha 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                             C4-type.
PH 1.
PH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
Pfam; PF00169; PH; 2.
PRINTS; PR00405; REVINTRACTNG.
SMART; SM00105; ArfGap; 1.
SMART; SM00233; PH; 2.
PROSITE; PS50115; ARFGAP; 1.
PROSITE; PS50003; PH_DOWAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                        48
232
360
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                   131
254
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGEN
                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEA2_HUMAN
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Page
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us-10-614-959-15.rup

COO7 47.60.07

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.R., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). INTERACTION WITH PTDINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
PubMed=14690521; 2

Hanck T., Stricker R., Sedehizade F., Reiser G., Identification of gene structure and subcellular localization of human centaurin alpha 2, and p42IP4, a family of two highly homologous, Ins 1,3,4,5-P4-/Ptdins 3,4,5-P3-binding, adapter

affinity.
SUBCELLUIAR LOCATION: Cytoplasmic. Constitutively associated with the plasma membrane. Excluded from the nucleus.
ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2; Name=1;

IsoId=Q9NPF8-1; Sequence=Displayed;

Isold=ONNPPB-2; Sequence=VSP_011180;
Note=May be due to a competing acceptor splice site. No
experimental confirmation available;
-1- TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney,
skeletal muscle and adrenal gland. Weakly expressed in thyroid,
liver, heart, lung, small intestine, peripheral blood leukocytes.
Not detected in spinal cord, brain, stomach, trachea, colon, lymph
node and bone marrow.
-1- SIMILARITY: Contains 1 Arf-GAP domain.

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EMBL, AJ238994; CAB88383.1; -EMBL, AJ272195; CAB77266.1; -EMBL, BC033758; CAG40651.1; -EMBL, BC033758; AAH33758.1; -H.INVDB, HIXO013699; -HIXON HIXO013699; -INTERPRO; IPRO01164; HRIP_like.
INTERPRO; IPRO11036; PH.
Fam; PPO1412; ArfGap; I.
Pfam; PPO1412; ArfGap; I. 

PROSITE; PS50115; ÄRFGAP; 1. PROSITE; PS50003; PH DOMAIN; 2. Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger. PRINTS: PRO0405; REVINTRACTING. SMART; SM00105; ArfGap; 1. SMART; SM00233; PH; 2.

Gapa ö Query Match
69.0%; Score 40; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels /FTId=VSP_011180. L -> P (in Ref. 3). MW; 4FAE208072A92C01 CRC64; Arf-GAP.
C4-type.
PH 1.
PH 2.
Missing (in isoform 2). 12 12 381 AA; 44348 3 WDDSLSEFL 11 25 132 255 269 DOMAIN ZN FING DOMAIN DOMAIN CONFLICT 57777778 ઠે

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||||: ||: 69 WDDSIVEFM 77

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Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090; 25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Centaurin alpha 2. PRT; 381 AA STANDARD; Name=Centa2; MOUSE RESULT 10 CEA2_MOUSE ID CEA2_MOU AC Q8R2V5;

RN SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Breast tumor;

RX MEDLINE=21886257; PubMed=12477952; DOI=10.1073/pnas.24563999;

RX MEDLINE=22886257; PubMed=12477952; DOI=10.1073/pnas.24563999;

RX Altaenberg R.L., Fehigodd E.A., Grouse L.H., Derge J.G.

RA Altenbul S.P., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altenbul S.P., Zebergg B., Bustow K.H., Schaefer C.P., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Haich F. N.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Staba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

RA Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Glubs R.A.,

RA Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Glubs R.A.,

RA Winting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Minting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C. Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and modifical analysis of more than 15,000 full-length human and most of U.S.A., 99:16999-16903(2002)

"Froc. Natl. Acad. Sci. U.S.A., 99:1699-16903(2002)

"Froc. Natl. Bands phosphatidylinosttol 3,4,5-trisphosphate (PtdInsP3)

and inositol 1,3,4,5-tetrakisphosphate (Torphy Mith identical affinity (By similarity).

"FUNCTION: CTPase-activating protein for the ADP ribosylation affinity (By similarity).

"FUNCTION: CTPASS CORTAINS 1,2000 decortic the plasma membrane Excluded from the nucleus (By similarity).

"SIMILARITY: Contains 1 2 PH domains. 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SU47 / 1021;
MEDLINE=SU47 / 1021;
MEDLINE=SU21023; PubMed=9922248;
MEDLINE=99121023; PubMed=9922248;
MPOLY=1-Vydroxybutyrate degradation in Rhizobium (Sinorhizobium)
mellloti: isolation and characterization of a gene encoding 3-
mellloti: isolation and characterization of a gene encoding 3-
Macrostucyrate dehydrogenase.";
J. Bacteriol. 181:849-857(1999)
--- FUNCTION: Key enzyme in the regulation of glycerol uptake and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC027165; AAH27165.1; -.

MGD; MGI:2663075; Centa2.

A InterPro; IPR001164; hRIP_like.

InterPro; IPR001164; bH.

InterPro; IPR01036; PH. related.

R pfam; PP00169; PH; 2.

R PRAT; SM00105; ArfGap; 1.

R SWART; SM00105; ArfGap; 1.

R RSWART; SM00105; ArfGap; 1.

R ROSITE; PS50013; PH DOWAIN; 2.

R ROSITE; PS50013; PH DOWAIN; 2.

R GTPase activation; Metal-binding, Repeat; Zinc-finger.

DOWAIN 25 48 C4-type.

T ZN FING 25 48 C4-type.
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-!- PATHWAY: Glycerol utilization; rate-limiting step.
-!- SIMILARITY: Belongs to the fucokinase / gluconokinase / glycerokinase / xylulokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolism.
-!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 66.7%; Score 40; DB 1; Length 381; 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             25 48 C4-Cype.
132 233 PH 1.
255 361 PH 2.
381 AA, 43989 MW, 2ESO4CEFOACD84D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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086033;
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                                                                                               EMBL; AL591985; CAC49535.1; -.
EMBL; AP080548; AAD12735.1; -.
EMBL; AP080548; AAD12735.1; -.
HNSP; P08859; 1GLG.
HAMP; MF_00186; -; 1.
InterPro; IPR000579; Glycerol_kin.
InterPro; IPR00599; Glycerol_kin.
Pfam; PF00370; FGGY C; 1.
Pfam; PF00370; FGGY C; 1.
Pfam; PF00370; FGGY C; 1.
PROSITE; PS00933; FGGY KINASES 1; FALSE_NEG.
PROSITE; PS00445; FGGY KINASES 2; 1.
ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
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60.0%; Pred. No. 91;
iive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Juerchott K., Boerner T.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-12>2) ...
EMBL; Z28337; CAA62191.1; -.
PIR; S49113; S49113.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR000345; CytC_heme_BS.
From: PP05272; VirE; 1.
Ffan; PP05272; VirE; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                153 165 ATP (Probable).
497 AA; 54419 MW; 42D342B335ACC2B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Putative helicase C28H8.3 (EC 3.6.1.-).
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les 6; Conserv
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YP93_CAREL
ID YP93_CAEEL
AC Q09475;
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Q48904;
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Matches
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Q48904
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MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 282:2012-2018(1998). 69.0%; Score 40; DB 1; Length 1714; 88.9%; Pred. No. 3.4e+02; Live 0; Mismatches 1; Indels EMBL, U20861; AA62291.2;

WormBase; WBGene00016194; C28H8.3.

WormPep; C28H8.3; CE29195.

InterPro; IPR001410; DBEAD.

InterPro; IPR001650; Helicase_C.

Pfam; PF00270; Helicase_C; 1.

SNART; SM00490; HELICc; 1.

SNART; SM00490; HELICc; 1.

TIGRFAMS; TIGR01870; cas_TM1810; 2.

ATP-binding; Helicase; Hydrolase; Hypothetical protein;

Nuclear protein.

NP BIND 607 614 ATP (Potential).

NP BIND 806 813 ATP (Potential).

SITE 913 916 BEWH box. 806 813 ATP (FOCESSILLAL). 913 916 DEVH box. 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64; Local Similarity 88.9 NCBI_TaxID=6239; SEQUENCE FROM N.A. Waterston R.; [2] REVISIONS. SEQUENCE Query Match 

5 AAWDDSDSE 13 1 AAWDDSLSE 9 RESULT 14 셤 ઠે

DYHC NEUCR STANDARD; PRT; 4367 AA. P45443; Q7RVH1; 01-NOV-1995 (Rel. 32, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Dynein heavy chain, cytosolic (DYHC). DYHC_NEUCR ID DOT DOT SERVICE SER

Neurospora crassa. Bukaryota; Wordy, Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. NCBI_TaxID=5141;

STRAIN=74-0R23-1M, / FGSC 987;
MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.139;
Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.;
"Cytoplasmic dynein and actin-related protein Arp1 are required for SEQUENCE FROM N.A.

REARINE-4-0213-1A, FGSC 987;
REARINE-4-0213-1A, FGSC 987;
REARINE-4-0213-1A, FGSC 987;
REARINE-4-0213-1A, FGSC 987;
RAARINE-4-0213-1A, FGSC 987;
RAARINE-4-0212-10-10.198/nature01554;
Radagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Elkins T., Engels R., Wang S., Nielsen M.A.,
RA Elkins T., Engels R., Wang S., Nielsen M.A.,
RA Eleis G., Greenberg D., ROY A., Folly W., Nalylor J.,
RA Marcotte E., Greenberg D., ROY A., Folly W., Nalylor J.,
RA Marcotte E., Metzenberg B., Frishman D., Kryetofowa S.,
RA Marcotte E., Metzenberg B.L., Perkins D. D., Kroken S., Cogoni C.,
RA Machin G., Carcheside D. Li W., Pratt R.J., Osmani S.A.,
RA Marcotte E., Metzenberg R.L., Perkins D. D., Kroken S., Cogoni C.,
RA Marcotte E., Metzenberg R.L., Perkins D.J., Nalylor J.,
RA Marcotte E., Metzenberg E., Nannhaup J., Nadord S.,
RA Marcotte E., A., Mannhaupt G., Ebbole D.J., Frattag M.,
RA Marci D., Alex L.A., Mannhaupt G., Ebbole D.J., Frattag M.,
RA Marcotte E., A., Mannhaupt G., Ebbole D.J., Frattag M.,
RA Marcotte E., A., Mannhaupt G., Ebbole D.J., Frattag M.,
RA Marcotte E.S., Nusbaum C., Birren B.,
Mature 422.859-868(2003).
LI Wature 422.859-868(2003).
LI FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular retrogerade motility of vesicles and organelles along microbules.
Dynain has APase activity; the force-producing power stroke is bynein has APases activity; the force-producing power stroke is bynein has APases activity; the force-producing power stroke is bynein has APases activity; the force-producing power stroke is nuclear distribution in hyphae.

LI FUNCTION: Cytoplasmic dynains and a number of nuclear distribution in hyphae.

LI SUBUNIT: Consists of at least two heavy chains and a number of which binds cargo and lineraced with one per AAA domains in the head or motor domain. T rmal nuclear distribution in filamentous fungi."; Cell Biol. 127:139-149(1994).

SIMILARITY: Belongs to the dynein heavy chain family.

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EMBL, L31564; AAA64908.1; -.
EMBL, AABX0L000204; EAA33380.1; -.
PIR, B54802; B54802.
InterPro, IRR033533; AAA ATPase.
InterPro, IRR034273; Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
SmART; SM00382; AAA, 3.
ATP-binding; Colled call; Dynein; Microtubule; Motor protein; Repeat. AMA 1 (By similarity).
AMA 1 (By similarity).
AMA 3 (By similarity).
AMA 4 (By similarity).
AMA 4 (By similarity).
Stalk (By similarity).
Stalk (By similarity).
AMA 5 (By similarity).
AMA 6 (By similarity).
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Coiled coil (Potential). 1904 2130 2460 2815 3179 3481 4215 693 19905 22202 22506 23909 3193 3565 4003 676 11327 DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN

8 1/3 1/2 1/4 1/4 1/4 1/4

us-10-614-959-15.rup

ORFNames=C28H8.3

(Potential)

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SEROIDENE FROW N.A.
SEROIDENE FROW N.A.
STRAINENEMD 2210633 / Serotype 03:K6;
MEDLINE-22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
MEDLINE-22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima W., Nakano W., Yamashitea A., Kubota Y., Tagomori K.,
Iljima Y., Najima M., Nakano M., Yamashitea A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Ilda T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 1361:74-749(2003).
EMBL; AP005088; BAC62555.1; -.
Complete protecome; Hypothetical protein.
SEQUENCE 182 AA; 21333 MW; 2559BEC89FD78332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                               Gaps
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0 08/GV3;

1 01-JUN-2003 (TrEMBLrel. 24, Created)

1 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

1 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

1 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

1 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

2 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

3 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

4 07-JUN-2003 (TrEMBLrel. 24, Last annotation update)

5 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

6 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

7 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

8 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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                                                                                                                                                                                                       Score 40; DB 1; Length 4367;
Pred. No. 9.3e+02;
2; Mismatches 1; Indels
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                                                                                                                                                    ATP (Potential).
MW; 1E10F3E2D170D6DF CRC64;
                       (Potential).
(Potential).
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Coiled coil (Poten
ATP (Potential).
ATP (Potential).
ATP (Potential).
   1637 1668
3195 2218
3193 3296
3423 3481
3778 3809
1377 1950
2240 2247
2505 2612
2605 2612
267 264
4367 268 M
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Best Local Similarity 66.7%;
Matches 6; Conservative
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